

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 22.2289 Seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179a-2
Perfect score: 341
Sequence: 1 KDRPFCBLPDTGRCVRV.....CEGNANPTKEECSTCA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341	100.0	83	13	Q90WAI pseudonaja
2	322	94.4	83	13	Q90WAO pseudonaja
3	245	71.8	83	13	Q90W99 pseudonaja
4	241	70.7	83	13	Q90W98 pseudonaja
5	241	70.7	83	13	Q90W96 pseudonaja
6	226	66.3	83	13	Q90W97 pseudonaja
7	202	59.2	88	13	Q8AY43 bungarus ca
8	198	58.1	58	13	Q9TW99 anemonia su
9	190	55.7	59	5	Q9TW98 anemonia su
10	189	55.4	88	13	Q8AY42 bungarus ca
11	187.5	55.0	76	5	Q8T719 bombyx mori
12	185	54.3	58	5	Q9TW90 anemonia su
13	185	54.3	86	5	Q9GP15 ixodes ric
14	183	53.7	88	11	Q8AY41 bungarus ca
15	183	53.7	230	11	Q8CP99 ratius norv
16	182.5	53.5	80	5	Q8T367 araneus ven

17	181	53.1	984	5	Q9GON2 calliacis
18	181	53.1	984	5	Q9GON1 calliacis
19	178	52.2	142	5	Q8WP12 boophilus m
20	175	51.3	142	5	Q8WP13 boophilus m
21	172	50.4	759	5	Q8IT91 ancylostoma
22	171.5	50.3	57	5	Q8MTR6 haematobia
23	171	50.1	113	5	Q9V508 drosophila
24	169	49.6	235	11	Q8CI80 mus musculu
25	169	49.6	235	11	Q8BSB7 canis famil
26	169	49.6	396	6	Q28874 canis famil
27	168	49.3	79	13	Q9I351 dendroaspis
28	163	47.8	132	5	Q9VGT9 drosophila
29	163	47.8	195	11	Q9D8Q8 mus musculu
30	162	47.5	1572	5	Q44938 haemochus
31	161	47.2	576	4	Q8TEU8 homo sapien
32	160	46.9	548	4	Q96N28 homo sapien
33	160	46.9	979	4	Q8N421 homo sapien
34	160	46.9	3198	5	Q9U8G8 manduca sex
35	158	46.3	82	5	Q8MVB4 ixodes ricap
36	157	46.0	222	11	Q8R0S6 mus musculu
37	157	46.0	222	11	Q8R0S6 mus musculu
38	156.5	45.9	76	5	Q96S88 gallieria me
39	156	45.7	137	6	Q9BD10 dryocollagus
40	155	45.5	738	13	Q90W28 drachydantio
41	154	45.2	461	5	Q9S622 drosophila
42	154	45.2	747	13	Q91963 xenopus. ap
43	154	45.2	763	5	Q9XZD0 drosophila
44	153	44.9	133	6	Q8HZ45 papio papio
45	152	44.6	169	6	Q9NOX7 bos taurus

ALIGNMENTS

RESULT 1

ID	Q90WAI	PRELIMINARY;	PRT;	83 AA.
AC	Q90WAI			
DT	01-DEC-2001	(TEMBLrel. 19, Created)		
DT	01-DEC-2001	(TEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003	(TEMBLrel. 23, Last annotation update)		
DE	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Elapidae; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TTSUB=Venom gland;			
RA	Whitaker A.N., Gaffney P.J., Sorokina I.N., Filipovich I.V.,			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF402324; AAK95519.1; -			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI.1.			
DR	ProDom; PD000222; Kunitz_BPTI.1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Protease inhibitor; Serine protease inhibitor.			
SQ	SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;			
Query Match	100.0%;	Score 341;	DB 13;	Length 83;
Best Local Similarity	100.0%;	Pred. No. 1.3e-36;		
Matches 59;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 2

Q90W90 PRELIMINARY; PRT; 83 AA.
 AC Q90W90; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9179 MW; 67B589AD7175930 CRC64;

Query Match 94.4%; Score 322; DB 13; Length 83;
 Best Local Similarity 93.2%; Pred. No. 3.7e-34;
 Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 3

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF402326; AAK95521.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9158 MW; 36BEB82487ACFB61 CRC64;

Query Match 71.8%; Score 245; DB 13; Length 83;
 Best Local Similarity 67.8%; Pred. No. 3.6e-24;
 Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 4

Q90W98 PRELIMINARY; PRT; 83 AA.
 AC Q90W98; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.
 NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF402327; AAK95522.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 8983 MW; 3F28548146548A9B CRC64;

Query Match 70.7%; Score 241; DB 13; Length 83;
 Best Local Similarity 71.2%; Pred. No. 1.2e-23;
 Matches 42; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 59
 Db 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCKLEFIYGGCGGNANFTTKCESTCA 83

RESULT 5

Q90W96 PRELIMINARY; PRT; 83 AA.
 AC Q90W96; 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Textlinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavlin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RT "Plasma in inhibitors from the Australian brown snake Pseudonaja
RT textilis textilis."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavlin M.F.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL/A402229; AAK95348.1;
DR InterPro; IP0002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI.
DR SMART; SM00131; KU. 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR Kunitz inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9060 MW; A66DF2692864C58E CRC64;

Query Match 70.7%; Score 241; DB 13; Length 83;
Best Local Similarity 71.2%; Pred. No. 1.2e-23;
Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

1 KDRPFCBLPADIPGCRVPRPSPFYNNDEKKCLEFIYGGCGGNANNNFTKKECESTCA 59
25 KDRPFCBLPADIPGCRVPRPSPFYNNDEKKCLEFIYGGCGGNANNNFTKKECESTCA 83

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DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9031 MW; 9CAA7FE390D9B191 CRC64;

Query Match 66.3%; Score 226; DB 13; Length 83;
Best Local Similarity 67.8%; Pred. No. 1e-21;
Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

1 KDRPFCBLPADIPGCRVPRPSPFYNNDEKKCLEFIYGGCGGNANNNFTKKECESTCA 59
25 KDRPFCBLPADIPGCRVPRPSPFYNNDEKKCLEFIYGGCGGNANNNFTKKECESTCA 83

RESULT 7
ID Q8AY43 PRELIMINARY; PRT; 88 AA.
AC Q8AY43;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Kunitz inhibitor a (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Teal I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus."
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057886; AAL30068.1;
DR NON_TER 1 1
SQ SEQUENCE 88 AA; 9606 MW; E2C089906909563D CRC64;

Query Match 59.2%; Score 202; DB 13; Length 88;
Best Local Similarity 56.9%; Pred. No. 1.4e-18;
Matches 33; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

1 KDRPFCBLPADIPGCRVPRPSPFYNNDEKKCLEFIYGGCGGNANNNFTKKECESTCA 58
30 KDRPFCBLPADIPGCRVPRPSPFYNNDEKKCLEFIYGGCGGNANNNFTKKECESTCA 87

RESULT 8
ID Q9TWP9 PRELIMINARY; PRT; 58 AA.
AC Q9TWP9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE KALICUDINE 2, ASKC2.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinoptaria;
OC Nymphaeae; Actinidae; Anemona.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.
RC MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemane B., Moinier D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicudines and kalieptins. Two different classes of sea anemone
RT toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSSP; P12111; 2KNT.
DR InterPro; IP0002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI.
DR SMART; SM00131; KU. 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

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KW Peptase inhibitor; Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6778 MW; F102E71682F1A55C CRC64;

Query Match 58.1%; Score 198; DB 5; Length 58;
Best Local Similarity 62.7%; Pred. No. 3.1e-18;
Matches 32; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKCECSTC 57
Db 5 CLPMDVGRCAARHPRFYNNSSRRCCKFTYGGCGGNANNFITKCECKVC 55

RESULT 9

Q9TW8 PRELIMINARY; PRT; 59 AA.

AC O9TW8; 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE KALICUDINE 3, ASKC3.
OS Anemoma sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anemoma.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.

RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemaire E., Moirier D., Lancelin J.M.,
Beres L., Lazdunski M.;
RT "Kalicudines and kalieptine. Two different classes of sea anemone
toxins for voltage sensitive K⁺ channels.";
RL J. Biol. Chem. 270:25121-25126(1995).

DR HSP; P31713; ISHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR PRINTS; PR00759; BASICPASE.
DR ProDom; PD000222; Kunitz_BPTI.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394DA5 CRC64;

Query Match 55.7%; Score 190; DB 5; Length 59;
Best Local Similarity 62.7%; Pred. No. 3.4e-17;
Matches 32; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKCECSTC 57
Db 5 CELPKVGRCAARHPRFYNNSSRRCCKFTYGGCGGNANNFITLCECKVC 55

RESULT 10

Q8AY42 PRELIMINARY; PRT; 88 AA.

AC O8AY42; 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Kunitz inhibitor b (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;
RA Test I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057887; AAL30069.1; -.
FT NON_TER 1 1

SQ SEQUENCE 88 AA; 9391 MW; 71P9F57D36E7A652 CRC64;

Query Match 55.4%; Score 189; DB 13; Length 88;
Best Local Similarity 54.4%; Pred. No. 6.9e-17;
Matches 31; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KDRPFCLEPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKCECSTC 57
Db 30 KDRKFCVPRPBRNANVAFYNNPRLRACIEFTYGGCGGNANNFSGGCKKAC 86

RESULT 11

Q8T7L9 PRELIMINARY; PRT; 76 AA.

AC Q8T7L9; 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Kazal-type serine proteinase inhibitor 1.
GN Spil.

OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dityria; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21873253; PubMed=11861808;
RA Nirmala X., Mita K., Vanistree V., Zurovec M., Sehgal F.;
RT "Identification of four small molecular mass proteins in the silk of
Bombyx mori.";
RL Insect Mol. Biol. 10:437-445(2001).
DR EMBL; AF352583; AAL63944.1; -.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR ProDom; PD000222; Kunitz_BPTI.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 76 AA; 8445 MW; AA3F97D373535A3B CRC64;

Query Match 55.0%; Score 187.5; DB 5; Length 76;
Best Local Similarity 61.1%; Pred. No. 9.4e-17;
Matches 33; Conservative 6; Mismatches 14; Indels 1; Gaps 1;

Qy 4 PDFCELPADTGPCRVPRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKCECSTC 57
Db 23 PD-CLPDKTGPCRSPFRVAYDSBCKVCFIYGGCGGNANNFITIECEAAC 75

RESULT 12

Q9TWG0 PRELIMINARY; PRT; 58 AA.

AC Q9TWG0; 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE KALICUDINE 1, ASKC1.
OS Anemoma sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anemoma.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.

RX MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemaire E., Moirier D., Lancelin J.M.,
Beres L., Lazdunski M.;
RT "Kalicudines and kalieptine. Two different classes of sea anemone
toxins for voltage sensitive K⁺ channels.";
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P10646; IADZ.
DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 58 AA; 6691 MW; 253806896B4BDCD CRC64;

Query Match 54.3%; Score 185; DB 5; Length 58;
 Best Local Similarity 60.8%; Pred. No. 1.5e-16;
 Matches 31; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 7 CELPADTGPCRVPRPSFYNNPDEKKCLEFYGGCGGNANNFITKECESTC 57
 Db 5 CLPMDVGRCAHPRYYNSSSRCKRFTYGGCGGNANNFITKECEKVC 55

RESULT 13

ID O9GP15 PRELIMINARY; PRT; 86 AA.
 AC O9GP15;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical 9.7 kDa protein.
 OS Ixodes ricinus (castor bean tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
 OX NCBI_TaxID=34613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Lebouille G., Rochez C., Louahed J., Rutti B., Brosseard M., Bollen A.,
 RA Godfroid E.;
 RT "Isolation of Ixodes ricinus salivary gland mRNAs encoding factors
 RT induced during the blood feeding process."
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ269641; CAB55816.1; -
 DR HSSP; P12111; IKRT.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 86 AA; 9727 MW; 9473B17974A055F0 CRC64;

Query Match 54.3%; Score 185; DB 5; Length 86;
 Best Local Similarity 52.5%; Pred. No. 2.2e-16;
 Matches 31; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 KDRPFCPLPADTGPCRVPRPSFYNNPDEKKCLEFYGGCGGNANNFITKECESTCA 59
 Db 25 KGRPAKCKLPDDGCRARIPSYIFDRKTKCKEPRFYGGCGGNANNFENITTCQECNA 83

RESULT 14
 ID O8AY41 PRELIMINARY; PRT; 88 AA.

AC O8AY41;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Kunitz inhibitor c (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=92438;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057888; AAJ30070.1; -
 FT NON_TER
 SQ SEQUENCE 88 AA; 9659 MW; 0279950755F6B787 CRC64;

Query Match 53.7%; Score 183; DB 13; Length 88;
 Best Local Similarity 56.9%; Pred. No. 4.2e-16;
 Matches 33; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KDRPFCPLPADTGPCRVPRPSFYNNPDEKKCLEFYGGCGGNANNFITKECESTCA 58
 Db 30 KNRPFNCNLPBPRCAIVRAFYNNRLKRCLEFPYGGCGGNANNFITIDCQRTCA 87

RESULT 15

ID O8CF99 PRELIMINARY; PRT; 230 AA.
 AC O8CF99;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Tissue factor pathway inhibitor-2 precursor.
 GN TPPI-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Placenta;
 RA MEDLINE=22183372; PubMed=12195712;
 RA Hsaka T., Kistiel W., Rosenbaum U.;
 RT "cDNA cloning and tissue distribution of the rat ortholog of tissue
 RT factor pathway inhibitor-2."
 RL Thromb. Haemost. 88:356-357(2002).
 DR EMBL; AJ28954; CND22046.1; -
 KW Signal.
 FT SIGNAL
 FT CHAIN
 SQ SEQUENCE 230 AA; 26157 MW; 07CD5B9F7D43ED9 CRC64;

Query Match 53.7%; Score 183; DB 11; Length 230;
 Best Local Similarity 56.6%; Pred. No. 1.1e-15;
 Matches 30; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 5 DFCPLPADTGPCRVPRPSFYNNPDEKKCLEFYGGCGGNANNFITKECESTC 57
 Db 34 EICLPDMDGFCALIKFYIDRQKCRKRKYGCGGNANNFHRSKCKCHTC 86

Search completed: January 23, 2004, 10:27:15
 Job time : 24.289 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 28.4613 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179a-2
Sequence: 1 KORPDCFLPADTGPCRVRP.....CEGNANPITRECESTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341	100.0	59	21	AAV15138
2	341	100.0	60	21	AAV15145
3	334	97.9	60	21	AAV15153
4	322	94.4	59	21	AAV15139
5	322	94.4	83	21	AAV15146
6	298	87.4	60	21	AAV15154
7	245	71.8	59	21	AAV15140
8	245	71.8	83	21	AAV15147
9	227	66.6	59	21	AAV15143

10	227	66.6	83	21	AAV15150
11	226	66.3	59	21	AAV15142
12	226	66.3	83	21	AAV15149
13	225	66.0	59	21	AAV15141
14	225	66.0	83	21	AAV15148
15	221	64.8	58	17	AAV15146
16	201	58.9	58	16	AAV15144
17	196	57.5	58	16	AAV15145
18	192	56.3	58	16	AAV15147
19	189	55.4	58	16	AAV15143
20	185	54.3	86	22	AAV15140
21	185	54.3	124	18	AAV15142
22	185	54.3	144	18	AAV15149
23	184	54.0	58	17	AAV15147
24	183	53.7	55	18	AAV15141
25	183	53.7	60	21	AAV15151
26	183	53.7	124	18	AAV15148
27	183	53.7	144	18	AAV15145
28	183	53.7	145	18	AAV15146
29	183	53.7	165	18	AAV15147
30	182	53.4	58	17	AAV15149
31	182	53.4	58	17	AAV15142
32	181	53.1	58	13	AAV15140
33	181	53.1	58	17	AAV15145
34	181	53.1	58	17	AAV15146
35	180	52.8	58	13	AAV15140
36	180	52.8	58	17	AAV15141
37	180	52.8	58	17	AAV15142
38	179	52.5	58	16	AAV15143
39	179	52.5	58	16	AAV15144
40	177	51.9	58	17	AAV15145
41	176	51.6	58	17	AAV15146
42	175	51.3	58	13	AAV15147
43	175	51.3	58	16	AAV15148
44	175	51.3	58	17	AAV15149
45	174	51.0	58	16	AAV15143

ALIGNMENTS

RESULT 1	AAV15138	AAV15138 standard; Protein; 59 AA.
XX	AAV15138;	
AC	AAV15138;	
XX		
DT	07-FEB-2000 (first entry)	
XX		
DE	Txln 1 Plasmin inhibitor protein.	
XX		
KW	Textilinin protein; Txln 1, plasmin inhibitor; single stage inhibitor;	
KW	Australian brown snake; conserved cysteine residue; stability; control;	
KW	haematopoietic; cytoskeletal activity; homology; specificity; Aprotinin;	
KW	Taurocorin-associated plasmin inhibitor; TAC; inhibitory efficiency;	
KW	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;	
KW	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;	
KW	reduced propensity; thrombosis.	
OS	Pseudonaja textilis textilis.	
XX		
PN	MO9958569-A1-7	
PD	18-NOV-1999.	
XX		
PF	07-MAY-1999; 99WO-AU00343.	
XX		
PR	11-MAY-1998; 98AU-0003450.	
XX		
PA	(UYOU) UNIV QUEBENS/LAND.	
PA	(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.	
PA	(MASC/) MASC P F.	
PA	(LAVI/) LAVIN M F.	

Proform of Txln 6
Txln 5 Plasmin inh
Proform of Txln 5
Txln 4 Plasmin inh
Proform of Txln 4
Aprotinin-like Kun
Human LACI-K2 deri
Human collagen alp
Human TPPI-2 domai
Human LACI-K3 deri
I. ricinus salivar
New protease inhib
SUC2-Bp7-d21-RPDP-
Genetically engine
RPDP-Kunitz domain
Plasmin inhibitor
New protease inhib
SUC2-Bp1-d21-RPDP-
Novel protease inh
Elastase inhibitor
Genetically engine
Human neutrophil e
Genetically engine
Genetically engine
Human TPPI-2 domai
Human LACI-K1 deri
Genetically engine
Genetically engine
Human neutrophil e
HKT B9 KUDOM deri
Genetically engine
Human LACI-K1 deri

PA (GAF/) GAFNEY P J.
 XX
 XX Macci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 PI
 XX WPI; 2000-039073/03.
 DR
 XX N-PSDB; AA229017.
 DR
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT
 XX agents -
 PS
 XX Claim 8a; Page 68; 112pp; English.
 XX
 CC The present sequence is the Textilinin protein, Txln 1, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 458 and
 CC 588 homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 59 AA;
 Query Match 100.0%; Score 341; DB 21; Length 59;
 Best Local Similarity 100.0%; Pred. No. 8.6e-34;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDRPDCFLPADTGPCRVRFPSFYNNPDKKCLEFIVGGCGGNANPFTKCESTCAA 59
 DB 1 KDRPDCFLPADTGPCRVRFPSFYNNPDKKCLEFIVGGCGGNANPFTKCESTCAA 59
 RESULT 2
 ID AAY15145 standard; Protein; 83 AA.
 AC AAY15145;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Proform of Txln 1 protein.
 XX
 XX Textilinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KW haematopoietic; cytostatic activity; homology; specificity; control;
 KW Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 KW
 XX Pseudonaja textilis textilis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= leader_peptide
 FT 25..83
 FT /label= Txln-1 protein
 FT /note= "Textilinin-1"
 FT
 XX
 XX WO9958569-A1.
 PN
 XX 18-NOV-1999.
 PD
 XX 07-MAY-1999; 99WO-AU00343.
 PE
 XX 11-MAY-1998; 98AU-0003450.
 PR
 XX (UYQU) UNIV QUEENSLAND.
 PA

PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 XX
 XX Macci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 PI
 XX WPI; 2000-039073/03.
 DR
 XX N-PSDB; AA229024.
 DR
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT
 XX agents -
 PS
 XX Claim 40a; Page 71; 112pp; English.
 XX
 CC The present sequence is the proform of the Textilinin protein, Txln 1,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 458 and
 CC 588 homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 83 AA;
 Query Match 100.0%; Score 341; DB 21; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.2e-33;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDRPDCFLPADTGPCRVRFPSFYNNPDKKCLEFIVGGCGGNANPFTKCESTCAA 59
 DB 25 KDRPDCFLPADTGPCRVRFPSFYNNPDKKCLEFIVGGCGGNANPFTKCESTCAA 83
 RESULT 3
 ID AAY15153 standard; Protein; 60 AA.
 AC AAY15153;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Plasmin inhibitor Txln 1, encoded by partial cDNA sequence.
 XX
 XX Textilinin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; homology; specificity; enzyme;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; cDNA;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW inhibitory efficiency; reduced propensity; thrombosis.
 KW
 XX Pseudonaja textilis textilis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 47
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"
 FT
 XX
 XX WO9958569-A1.
 PN
 XX 18-NOV-1999.
 PD
 XX 07-MAY-1999; 99WO-AU00343.
 PE
 XX

```

PR 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASC P P.
PA (LAVI/) LAVIN M F.
PA (GAF/) GAFFNEY P J.
PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
DR N-PSDB; AA229047.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
XX Disclosure; Fig 6; 112pp; English.
PS
XX The present amino acid sequence is the Txln 1, Textillin protein
XX encoded by the partial cDNA sequence. It is a single stage competitive
XX inhibitor of plasmin. It is isolated from the Australian brown snake,
XX Pseudonaja textilis textilis. Txln has high specificity for plasmin and
XX low inhibitory efficiency that can transiently affect the delicate
XX balance between enzymes and inhibitors of the fibrinolytic system,
XX controlling the fluidity of blood. The plasmin inhibitors are useful for
XX alleviating blood loss, following major surgery or trauma. Conjugates of
XX the plasmin inhibitor and an anti-fibrin antibody are useful as
XX anti-tumour agents. They have reduced propensity to cause thrombosis.
SQ Sequence 60 AA;
XX
XX Query Match 97.9%; Score 334; DB 21; Length 60;
XX Best Local Similarity 96.6%; Pred. No. 6.2e-33;
XX Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCAA 59
Db 2 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCGS 60
XX
XX RESULT 4
XX AAY15139
XX ID AAY15139 standard; Protein; 59 AA.
XX
XX AAY15139;
XX
XX 07-FEB-2000 (first entry)
XX
XX Txln 2 Plasmin inhibitor protein.
DE
XX Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytosolic activity; homology; specificity; Aptrothin;
XX Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
OS
XX WO958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.
XX (GAF/) GAFFNEY P J.

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XX
XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
PI WPI; 2000-039073/03.
XX
XX DR N-PSDB; AA229018.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
XX Claim 8b; Page 69; 112pp; English.
PS
XX The present sequence is the Textillin protein. Txln 2 that is a
XX single stage competitive inhibitor of plasmin. It is isolated from the
XX Australian brown snake, Pseudonaja textilis textilis. It has six
XX conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytosolic activity. Txln 2 has 43% and
XX 55% homology with Aptrothin and Taicotoxin-associated plasmin inhibitor
XX (TAC), respectively. Txln has high specificity for plasmin and low
XX inhibitory efficiency, that can transiently affect the delicate balance
XX between enzymes and inhibitors of the fibrinolytic system, controlling
XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
XX blood loss, following major surgery or trauma. Conjugates of the plasmin
XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
XX They have reduced propensity to cause thrombosis.
SQ Sequence 59 AA;
XX
XX Query Match 94.4%; Score 322; DB 21; Length 59;
XX Best Local Similarity 93.2%; Pred. No. 1.7e-31;
XX Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCAA 59
Db 1 KDRPDCFLPADTPGCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCAA 59
XX
XX RESULT 5
XX AAY15146
XX ID AAY15146 standard; Protein; 83 AA.
XX
XX AAY15146;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 2 protein.
DE
XX Textillin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; Aptrothin;
XX haematopoietic; cytosolic activity; homology; specificity; control;
XX Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX Protein /label= Leader_peptide
XX /label= Txln-2 protein
XX /note= "Textillin-2"
XX
XX WO958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

```

PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI: 2000-039073/03.
 DR N-PSDB; AA229025.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 PS Claim 40b; Page 71; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillin protein, Txln 2,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 2 has 43* and
 CC 5* homology with Aprotinin and Taticotxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 SQ Sequence 83 AA;
 XX
 Query Match 94.4%; Score 322; DB 21; Length 83;
 Best Local Similarity 93.2%; Pred. No. 2.5e-31;
 Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KDRPFCBLPADTGPCRVRFPSFYNNPDEKCLBFIYGGCEGNANFTTKBCESTCA 59
 Db 25 KDRPFCBLPADTGPCRVRFPSFYNNPDEKCLBFIYGGCEGNANFTTKBCESTCA 83
 RESULT 6
 AAY1514
 ID AAY1514 standard; Protein; 60 AA.
 XX
 AC AAY1514;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.
 XX
 KM Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytostatic activity; homology; enzyme;
 KM fluidity of blood; alleivate; blood loss; major surgery; trauma;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM inhibitory efficiency; reduced propensity; thrombosis.
 KM
 XX Pseudonaja textilis textilis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 45
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"
 FT Misc-difference 59
 FT /note= "encoded by CCN"
 XX
 XX W09958569-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-AU00343.

XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI: 2000-039073/03.
 DR N-PSDB; AA229048.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 PS Disclosure; Fig 7; 112pp; English.
 XX
 CC The present amino acid sequence is the Txln 2, Textillin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for
 CC alleviating blood loss, following major surgery or trauma. Conjugates of
 CC the plasmin inhibitor and an anti-fibrin antibody are useful as
 CC anti-tumour agents. They have reduced propensity to cause thrombosis.
 CC
 SQ Sequence 60 AA;
 XX
 Query Match 87.4%; Score 298; DB 21; Length 60;
 Best Local Similarity 89.5%; Pred. No. 1.4e-28;
 Matches 51; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KDRPFCBLPADTGPCRVRFPSFYNNPDEKCLBFIYGGCEGNANFTTKBCESTC 57
 Db 2 KDRPFCBLPADTGPCRVRFPSFYNNPDEKCLBFIYGGCEGNANFTTKBCESTC 58
 RESULT 7
 AAY15140
 ID AAY15140 standard; Protein; 59 AA.
 XX
 AC AAY15140;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Txln 3 Plasmin inhibitor protein.
 XX
 KM Textillin protein; Txln 3; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleivate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 KM
 XX Pseudonaja textilis textilis.
 OS
 XX
 PN W09958569-A1.
 PN 18-NOV-1999.
 PD 07-MAY-1999; 99WO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX
 XX (UYOU) UNIV QUEENSLAND.
 XX (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
 XX (MASC/) MASC P P.
 XX (LAVI/) LAVIN M F.
 XX (GAF/) GAFNEY P J.

XX (GAF/) GAFFNEY P. J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX MPI, 2000-039073/03.
 DR N-PSDB; AA229019.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 XX
 PS Claim 8c; Page 69; 112pp; English.
 XX
 CC The present sequence is the Textillinin protein, Txln 3, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 59 AA;
 Query Match 71.8%; Score 245; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 3.5e-22;
 Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 KDRPDCGLPADTGPCVRRPSPFYNDPEKKCLEFIYGGCGGNANPFITKECESTCA 59
 DB 1 KDRPDCGLPADTGPCVRRPSPFYNDPEKKCLEFIYGGCGGNANPFITKECESTCA 59
 RESULT 8
 AAY15147
 ID AAY15147 standard; Protein; 83 AA.
 XX
 AC AAY15147;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DB Proform of Txln 3 protein.
 XX
 KW Textillinin proform, Txln 3; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Leader_Peptide
 FT Protein 25..83
 FT /label= Txln-3_protein
 FT /note= "Textillinin-3"
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99MO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA

PA (GAF/) GAFFNEY P. J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX MPI, 2000-039073/03.
 DR N-PSDB; AA229026.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 agents -
 XX
 PS Claim 40c; Page 72; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillinin protein, Txln 3,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 83 AA;
 Query Match 71.8%; Score 245; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 5e-22;
 Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 KDRPDCGLPADTGPCVRRPSPFYNDPEKKCLEFIYGGCGGNANPFITKECESTCA 59
 DB 25 KDRPDCGLPADTGPCVRRPSPFYNDPEKKCLEFIYGGCGGNANPFITKECESTCA 83
 RESULT 9
 AAY15143
 ID AAY15143 standard; Protein; 59 AA.
 XX
 AC AAY15143;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DB Txln 6 Plasmin inhibitor protein.
 XX
 KW Textillinin protein, Txln 6; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Leader_Peptide
 FT Protein 25..83
 FT /label= Txln-3_protein
 FT /note= "Textillinin-3"
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99MO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFFNEY P. J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
 XX MPI, 2000-039073/03.
 DR N-PSDB; AA229022.
 DR

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XX XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX XX
PS Claim 8f, Page 69; 112pp; English.
XX
CC The present sequence is the Textillinin protein, Txln 6, that is a
CC single stage competitive inhibitor of plasmin. It is isolated from the
CC Australian brown snake, Pseudonaja textilis textilis. It has six
CC conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln has high
CC specificity for plasmin and low inhibitory efficiency, that can
CC transiently affect the delicate balance between enzymes and inhibitors
CC of the fibrinolytic system, controlling the fluidity of blood. The
CC plasmin inhibitors are useful for alleviating blood loss, following
CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC propensity to cause thrombosis.
CC
SQ Sequence 59 AA;

Query Match 66.6%; Score 227; DB 21; Length 59;
Best Local Similarity 67.8%; Pred. No. 5.2e-20;
Matches 40; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Oy 1 KDRPDCFLPADTGPCRVRFPSFYNNPDEKKCLEFIYGCCEGNANNFITKESCESTCAA 59
Db 1 KDRPFCFLPADIGPMDPTGAFHSPREHCIEFIYGCCKNANFNTOGECSTCAA 59

RESULT 10
AAV15150
ID AAV15150 standard; Protein; 83 AA.
AC AAV15150;
XX
DT 07-FEB-2000 (first entry)
XX
DE Proform of Txln 6 protein.
XX
XX Textillinin proform; Txln 6; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
OS Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-6_protein
FT /note= "Textillinin-6"
XX
XX MO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAFF/) GAFFNEY P J.
XX
XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
XX
XX WPI; 2000-039073/03.
XX

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DR N-PSDB; AA229029.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX XX
PS Claim 40f, Page 72; 112pp; English.
XX
CC The present sequence is the proform of the Textillinin protein, Txln 6,
CC from the Australian brown snake, Pseudonaja textilis textilis. It has
CC six conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln has high
CC specificity for plasmin and low inhibitory efficiency, that can
CC transiently affect the delicate balance between enzymes and inhibitors
CC of the fibrinolytic system, controlling the fluidity of blood. The
CC plasmin inhibitors are useful for alleviating blood loss, following
CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC propensity to cause thrombosis.
CC
SQ Sequence 83 AA;

Query Match 66.6%; Score 227; DB 21; Length 83;
Best Local Similarity 67.8%; Pred. No. 7.5e-20;
Matches 40; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Oy 1 KDRPDCFLPADTGPCRVRFPSFYNNPDEKKCLEFIYGCCEGNANNFITKESCESTCAA 59
Db 25 KDRPFCFLPADIGPMDPTGAFHSPREHCIEFIYGCCKNANFNTOGECSTCAA 83

RESULT 11
AAV15142
ID AAV15142 standard; Protein; 59 AA.
AC AAV15142;
XX
DT 07-FEB-2000 (first entry)
XX
DE Txln 5 Plasmin inhibitor protein.
XX
XX Textillinin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
OS Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-5_protein
FT /note= "Textillinin-5"
XX
XX MO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAFF/) GAFFNEY P J.
XX
XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV,
XX
XX WPI; 2000-039073/03.
XX
XX N-PSDB; AA229021.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
XX Claim 8e; Page 69; 112pp; English.
XX

```

XX The present sequence is the Textillinin protein, Txln 5, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

CC Sequence 59 AA;

Query Match 66.3%; Score 226; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 6.9e-20;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 KDRPDCLELPADPGPCVRFRFPFYNDPEKKCLEFIYGGCGGNANPITKECESTCA 59
 Db 1 KDRPDCLELPADPGPCVRFRFPFYNDPEKKCLEFIYGGCGGNANPITKECESTCA 59

RESULT 12

AA15149 standard; Protein: 83 AA.

AA15149;

07-FEB-2000 (first entry)

Proform of Txln 5 protein.

XX Textillinin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

XX Key Location/Qualifiers

FT Peptide 1..24 /label= Leader_peptide

FT Protein 25..83 /label= Txln-5 protein

FT /note= "Textillinin-5"

XX MO9958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

XX (GAFN/) GAFFNEY P J.

XX Mascal PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV,

XX WPI: 2000-039073/03.

XX N-PSDB; AA229028.

PS Claim 40e; Page 72; 112pp; English.

XX The present sequence is the proform of the Textillinin protein, Txln 5,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX Sequence 83 AA;

Query Match 66.3%; Score 226; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 9.9e-20;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 KDRPDCLELPADPGPCVRFRFPFYNDPEKKCLEFIYGGCGGNANPITKECESTCA 59
 Db 25 KDRPDCLELPADPGPCVRFRFPFYNDPEKKCLEFIYGGCGGNANPITKECESTCA 83

RESULT 13

AA15141 standard; Protein: 59 AA.

AA15141;

07-FEB-2000 (first entry)

Txln 4 plasmin inhibitor protein.

XX Textillinin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

XX MO9958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

XX (GAFN/) GAFFNEY P J.

XX Mascal PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV,

XX WPI: 2000-039073/03.

XX N-PSDB; AA229020.

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor

XX agents -

Claim 8d; Page 69; 112pp; English.

XX The present sequence is the Textillinin protein, Txln 4, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This

CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX Sequence 59 AA;

Query Match 66.0%; Score 225; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 9.1e-20;

Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGCRRRPFSPFYNNPDEKCLLEPTIYGCGGNANNFTKECESTCAA 59
 DB 1 KDHPRFCFLPARGTSCKGNVPRFYNNADHQLKPTIYGCGGNANNFTKECESTCAA 59

RESULT 14

AA15148
 ID AA15148 standard; Protein; 83 AA.

AC AA15148;

DT 07-FEB-2000 (first entry)

DE Proform of Txln 4 protein.

XX Textilin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

XX Key Location/Qualifiers

FT Peptide 1..24
 FT /label= leader_peptide
 FT Protein 25..83
 FT /label= Txln-4 protein
 FT /note= "Textilin-4"

XX MO9958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASI P P.

XX (LAVI/) LAVIN M F.

XX (GAFV/) GAFFNEY P J.

XX Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;

XX MPI; 2000-039073/03.

XX N-PSDB; AA220927.

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor

XX agents -
 XX Claim 40d; Page 72; 112pp; English.
 CC The present sequence is the proform of the Textilin protein, Txln 4,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has

CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX Sequence 83 AA;

Query Match 66.0%; Score 225; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 1.3e-19;

Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 KDRPFCFLPADTGCRRRPFSPFYNNPDEKCLLEPTIYGCGGNANNFTKECESTCAA 59
 DB 25 KDHPRFCFLPARGTSCKGNVPRFYNNADHQLKPTIYGCGGNANNFTKECESTCAA 83

RESULT 15

AA99146
 ID AA99146 standard; protein; 58 AA.

AC AA99146;

DT 12-FEB-1997 (first entry)

DE Aprotinin-like Kunitz domain.

XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
 KW smoke emphysema.

XX Synthetic.

XX WO9620278-A2.

XX 04-JUL-1996.

XX 15-DEC-1995; 95WO-US16349.

XX 16-DEC-1994; 94US-0358160.

XX (PROT-) PROTEIN ENG CORP.

XX Guterman SK, Kent RB, Ladhner RC, Ley AC, Markland W;

XX Roberts BL;

XX MPI; 1996-321851/32.

XX New engineered inhibitors of human neutrophil elastase - contg.
 PT aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or
 PT other respiratory disorders

XX Example 23; Page 47; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the
 CC elimination of pathogens and the restructuring of connective tissue.
 CC In cases of reduction of the circulating alpha-1-protease inhibitor
 CC (API or alpha antitrypsin), or the inactivation of API by oxidation
 CC (smoke emphysema), extensive destruction of the lung tissue may
 CC result from uncontrolled elastolytic activity of human neutrophil
 CC elastase. Other respiratory disorders such as cystic fibrosis are
 CC thought to be caused by human neutrophil elastase release by
 CC neutrophils. The genetically engineered human derived Kunitz
 CC domains can be used to treat such respiratory disorders. See

XX AA99146-R39211.

XX Sequence 58 AA;

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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 31.2711 Seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179A-22

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Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virius:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	97.4	83	13	Q90W98
2	372	81.2	83	13	Q90W99
3	341	74.5	83	13	Q90W01
4	333	72.7	83	13	Q90W00
5	332	70.3	83	13	Q90W96
6	317	69.2	83	13	Q90W97
7	282	63.6	88	13	Q8AY43
8	291	63.5	88	13	Q8AY41
9	279	60.9	88	13	Q8AY42
10	248	54.1	79	13	Q91351
11	214	46.7	90	13	Q8AY45
12	214	46.7	90	13	Q8AY44
13	193	42.1	90	13	Q8AY46
14	187	40.8	142	5	Q8WP12
15	184	40.2	142	5	Q8WP13
16	183	40.0	59	5	Q9TW98

17	183	40.0	85	13	Q9PTA4	Q9pta4 bungarus mu
18	180	39.3	85	13	Q9TW28	Q9tw28 bungarus mu
19	173	37.8	58	5	Q9TW60	Q9tw60 anemonia su
20	172.5	37.7	82	5	Q8MW04	Q8mw04 ixodes scap
21	172	37.6	76	5	Q8TW09	Q8tw09 bombyx mori
22	169	36.9	267	6	Q8MI34	Q8mi34 ovis aries
23	169	36.9	506	6	Q8MI33	Q8mi33 ovis aries
24	162	35.4	58	5	Q9TW99	Q9tw99 anemonia su
25	160	34.9	235	11	Q8CI80	Q8ci80 mus musculus
26	160	34.9	235	11	Q8BSB7	Q8bsb7 mus musculus
27	158	34.5	267	13	Q93424	Q93424 cyprinus ca
28	158	34.5	396	6	Q28874	Q28874 canis famli
29	155.5	34.0	80	5	Q8T357	Q8t357 areneus ven
30	154	33.6	1487	5	Q8MPV5	Q8mpv5 caenorhabdi
31	154	33.6	1558	5	Q8I710	Q8i710 caenorhabdi
32	154	33.6	2157	5	Q76840	Q76840 caenorhabdi
33	153.5	33.5	230	11	Q8CF99	Q8cf99 rattus norv
34	153	33.4	759	5	Q8IT91	Q8it91 ancylostoma
35	153	33.4	984	5	Q9GCON2	Q9gcn2 calliactis
36	153	33.4	984	5	Q9GCON1	Q9gcn1 calliactis
37	153	33.4	2225	5	Q45881	Q45881 caenorhabdi
38	152	33.2	169	6	Q9NOX7	Q9nox7 bos taurus
39	152	33.2	249	5	Q16701	Q16701 caenorhabdi
40	151.5	33.1	154	6	Q9NOX3	Q9nox3 ovis aries
41	151	33.0	277	13	Q8AYE1	Q8aye1 brachydanio
42	150	32.8	113	5	Q9V508	Q9v508 drosophila
43	150	32.8	167	4	Q8NE89	Q8ne89 homo sapien
44	150	32.8	224	4	Q8NAK6	Q8nak6 homo sapien
45	148	32.3	183	6	Q9NOX5	Q9nox5 bos taurus

ALIGNMENTS

RESULT 1

Q90W98 PRELIMINARY; PRT; 83 AA.

AC Q90W98;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Textillin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Acanthophinae; Pseudonaja.
 OX NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masai P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasma inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina N.I., Masai P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF402327; AAK95522.1;
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS02079; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor;
 SQ SEQUENCE 83 AA; 8983 MW; 3F28548146B4A9B CRC64;

Query Match 97.4%; Score 446; DB 13; Length 83;
 Best Local Similarity 97.6%; Pred. No. 8e-46;
 Matches 91; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSSGGLLLGLTMEVLTVPSSKDHKPFCELPARTGSCKGNVRFYNNADHOCLEFI 60
DB 1 MSSGGLLLGLTMEVLTVPSSKDHKPFCELPARTGSCKGNVRFYNNADHOCLEFI 60
QY 61 YGCGGANNPFTIEBKSTCA 83
DB 61 YGCGGANNPFTIEBKSTCA 83

RESULT 2
ID 090W99 PRELIMINARY; PRT; 83 AA.
AC 090W99;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Textillinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acantophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF402325; AAK95521.1; -
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9158 MW; 366EB2467ACB61 CRC64;

Query Match 81.2%; Score 372; DB 13; Length 83;
Best Local Similarity 79.5%; Pred. No. 5.9e-37;
Matches 66; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSSGGLLLGLTMEVLTVPSSKDHKPFCELPARTGSCKGNVRFYNNADHOCLEFI 60
DB 1 MSSGGLLLGLTMEVLTVPSSKDHKPFCELPARTGSCKGNVRFYNNADHOCLEFI 60
QY 61 YGCGGANNPFTIEBKSTCA 83
DB 61 YGCGGANNPFTIEBKSTCA 83

RESULT 3
ID 090W99 PRELIMINARY; PRT; 83 AA.
AC 090W99;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Textillinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acantophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF402324; AAK95519.1; -
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match 74.5%; Score 341; DB 13; Length 83;
Best Local Similarity 77.1%; Pred. No. 3.1e-33;
Matches 64; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSSGGLLLGLTMEVLTVPSSKDHKPFCELPARTGSCKGNVRFYNNADHOCLEFI 60
DB 1 MSSGGLLLGLTMEVLTVPSSKDHKPFCELPARTGSCKGNVRFYNNADHOCLEFI 60
QY 61 YGCGGANNPFTIEBKSTCA 83
DB 61 YGCGGANNPFTIEBKSTCA 83

RESULT 4
ID 090W99 PRELIMINARY; PRT; 83 AA.
AC 090W99;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Textillinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acantophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF402325; AAK95520.1; -
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9179 MW; 67B589AD27175930 CRC64;

Query Match 72.7%; Score 333; DB 13; Length 83;
Best Local Similarity 74.7%; Pred. No. 2.8e-32;

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Matches	62, Conservative	6, Mismatches	15, Indels	0, Gaps	0, Nucleotide
Qy	1	MSGGGLLLLLGLTLTMEVLTPTVSSSDHPKCEGLPAETGSCCKGNVRFYNNADHQCWPI	60		
Db	1	MSGGGLLLLLGLTLTMEVLTPTVSSSDRPBLCGLPDTGRCVRVPSFYNNPBGKCEPI	60		
Qy	61	YGGCGGANNPFTIEGKSTCA	83		
Db	61	YGGCGGANNPFTIEKCESTCA	83		

ID	Q90W96	PRELIMINARY;	PRT;	83 AA.
AC	Q90W96;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)			
DE	Textilinn.			
OS	Pseudonaja textilis textilis.			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Leiodontia; Squamata; Scleroglossa; Serpentes; Colubroidea;			
CC	Elapidae; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxId=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,			
RT	"Plasma inhibitors from the Australian brown snake Pseudonaja			
RL	textilis textilis."			
RN	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RA	TISSUE=Venom gland;			
RA	Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,			
RT	Whitaker A.N., Gaffney P.J., Lavin M.F.;			
RL	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF402339; AAK9348.1;			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI.1.			
DR	PRINTS; PR00759; BASICPTASE.			
DR	ProDom; PD000222; Kunitz_BPTI.1.			
DR	SMART; SMO0131; KU.1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
DR	Protease inhibitor; Serine protease inhibitor.			
QW	SEQUENCE 83 AA; 9060 MW; A66DF2692864C58E CRC64;			
Query Match	70.3%; Score 322; DB 13; Length 83;			
Best Local Similarity	72.3%; Pred. No. 5.9e-31;			
Matches	60; Conservative 7; Mismatches 16; Indels 0; Gaps 0			
QY	1 MSSGGLLLLLGLTMEVLTTPVSSKHDPKCELPARTGSCKNVDFPYNDHQCXRI 60			
DB	1 MSSGGLLLLLGLTMEVLTTPVSSKHDPKCELPADIGPCDDFTGAFHYSPREHCIEPI 60			
QY	61 YGGCGGNANPRTIEKSTCA 83			
DB	61 YGGCGGNANPRTIEKSTCA 83			

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OX  NCBI_TaxID=169397;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Venom gland;
RA  Masci P.P., Lavina M.F., Gaffney P.J., Sorokina I.N., Filpovich I.V.;
RT  "Plasmin inhibitors from the Australian brown snake Pseudonaja
RL  textilis textilis.";
RN  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RP  [2]
RC  SEQUENCE FROM N.A.
RC  TISSUE=Venom gland;
RA  Filpovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA  Whitaker A.N., Gaffney P.J., Lavina M.F.;
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RA  EMBL: AF402328, AAK55523.1;
DR  InterPro: IPR002223; Kunitz_BPTI.
DR  Pfam: PF00014; Kunitz_BPTI.1.
DR  Prodom: PD000222; Kunitz_BPTI.1.
DR  SMART: SM00331; KU.1
DR  PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR  PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW  Protease inhibitor; Serine protease inhibitor.
SQ  SEQUENCE 83 AA; 9031 MW; 9CAA7FE390D9B191 CRC64;
Query March 69.2% Score 317; DB 13; Length 83;
Best Local Similarity 72.3% Pred. No. 2,3e-30;
Matches 60; Conservative 8; Mismatches 15; Indels 0; Gaps 0.

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Query Match 69.2%; Score 317; DB 13; Length 83;
Best Local Similarity 72.3%; Pred. No. 2,36-30;
Matches 60; Conservative 8; Mismatches 15; Indels 0; Gaps 0.

Qy 1 MSSGGLLLIGLTLMEVLTPVSSKDPKPCELPAETGSCCKGNVPRFYNADHHOCLKFI 60
   |||||
Db 1 MSSGGLLLIGLTLMEVLTPVSSKDPKPCELPDGSCDFTGAFHYSTRDCEIEFI 60
   |||||

Qy 61 YGCGGNANFKTIEEGKSTCA 83
   |||||
Db 61 YGCGGNANFKTIEEGKSTCA 83
   |||||

RESULT 7
ID 08AY43 PRELIMINARY; PRT; 88 AA.
08AY43:
AC 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT Kunitz inhibitor a (Fragment).
DS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
NCBI TaxID=92438;
[1]
RN
RA TISSUE=Venom gland.
RC
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057886; ALU30068.1; -.
FT NON TER 1
SQ SEQUENCE 88 AA; 9606 MW; E2C089906909563D CRC64;

Query Match 63.8%; Score 292; DB 13; Length 88;
Best Local Similarity 68.3%; Pred. No. 2,46-27;
Matches 56; Conservative 5; Mismatches 21; Indels 0; Gaps 0.

Qy 1 MSSGGLLLIGLTLMEVLTPVSSKDPKPCELPAETGSCCKGNVPRFYNADHHOCLKFI 60
   |||||
Db 6 MSSGGLLLIGLTLCAELTPVSSKDPKPCVNPPEPGRCANVRAFYNPRLAKCIETFT 65
   |||||

Qy 61 YGCGGNANFKTIEEGKSTCA 82
   |||||
Db 66 YGCGGNANFKSNGECKRTCA 87
   |||||

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QY 1 MSSGGLLLGLTLTMEVLTTPVSS-KDHPKFCGLPAETGSCGNVPRFYNNADHHQCKF 59
DB 6 MSSGGLLLGLTLTMAELTTPVSSRKRPD-CDKPPDTRICQTVRAFYNNKPSARCKVCF 64
QY 60 IYGGCGGNANPKT 73
DB 65 RYGGCGNGNHPKS 78

RESULT 12

Q8AY44 PRELIMINARY; PRT; 90 AA.
AC Q8AY44;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta bungaratoxin B2D chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Teal I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057885; AAL30067.1; --
FT NON-TER
SQ SEQUENCE 90 AA; 10281 MW; 15754C179BDE190E CRC64;

Query Match 46.7%; Score 214; DB 13; Length 90;
Best Local Similarity 59.5%; Pred. No. 5.6e-18;
Matches 44; Conservative 8; Mismatches 20; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLTLTMEVLTTPVSS-KDHPKFCGLPAETGSCGNVPRFYNNADHHQCKF 59
DB 6 MSSGGLLLGLTLTMAELTTPVSSRKRPD-CDKPPDTRICQTVRAFYNNKPSARCKVCF 64
QY 60 IYGGCGGNANPKT 73
DB 65 RYGGCGNGNHPKS 78

RESULT 13

Q8AY46 PRELIMINARY; PRT; 90 AA.
AC Q8AY46;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta bungaratoxin B1 chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Teal I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057883; AAL30065.1; --
FT NON-TER
SQ SEQUENCE 90 AA; 10048 MW; E05C2A0D28179726 CRC64;

Query Match 42.1%; Score 193; DB 13; Length 90;
Best Local Similarity 56.8%; Pred. No. 1.8e-15;
Matches 42; Conservative 8; Mismatches 22; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLTLTMEVLTTPVSSKDHPKFCGLPAETGSCGNVPR-FYNNADHHQCKF 59

DB 6 MSSGGLLLGLTLTCAELTTPVSSRKRPDCKPPDKNC-GSVRAFYNNKPSARCKVCF 64
QY 60 IYGGCGGNANPKT 73
DB 65 RYGGCGNGNHPKT 78

RESULT 14

Q8WP12 PRELIMINARY; PRT; 142 AA.
AC Q8WP12;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Boophilin precursor.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RA Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
RA Wentele R., Huber R., Bode W., Fuentes-Prior P.;
RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
RT characterization, cloning and three-dimensional model of its complex
with thrombin";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Pereira P.J.;
RL Theais (1999), Universidade do Porto, Oporto, Portugal.
DR EMBL; AJ304447; CAC82583.1; --
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI_2.
DR PRINTS; PR00759; BASTCPYAS.
DR PRODOM; PD000222; Kunitz_BPTI_2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KM Protease inhibitor; Serine protease inhibitor; Signal.
FT SIGNAL
FT CHAIN 1 15
FT POTENTIAL.
FT BOOPHILIN, ISOFORM H2.
SQ SEQUENCE 142 AA; 15538 MW; 88BF0008BD42010 CRC64;

Query Match 40.8%; Score 187; DB 5; Length 142;
Best Local Similarity 57.4%; Pred. No. 1.5e-14;
Matches 31; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPATGSCGNVPRFYNNADHHQCKFYGGCGGNANPKTIEGKSTCA 83
DB 20 FCELPADGICAKLPFYNNKPSARCKVCF 73

RESULT 15

Q8WP13 PRELIMINARY; PRT; 142 AA.
AC Q8WP13;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Boophilin precursor.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.

RA Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
RA Wentele R., Huber R., Bode W., Fuentes-Prior P.;
RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
RT characterization, cloning and three-dimensional model of its complex
with thrombin";

```

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pereira P.J.;
RL Thesis (1999), Universidade do Porto, Oporto, Portugal.
DR EMBL; AJ304446; CAC82582.1; -.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR ProDom; PD000222; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Protease inhibitor; Serine protease inhibitor; Signal.
FT SIGNAL.
FT CHAIN 1 15 BOOPHTLIN, ISOFORM G2.
SQ SEQUENCE 142 AA; 1555 MW; EA6EC742D3599705 CRC64;

Query Match
Best Local Similarity 40.2%; Score 184; DB 5; Length 142;
Matches 30; Conservative 55.6%; Pred. No. 3.5e-14;
Mematches 16; Indels 0; Gaps 0;

QY 30 PCFLPAETGSCGNVPRFYTNADHHQCLFTYGGCGGNANPFTIEGKSTCA 83
DB 20 PCRLPADEGICKALIPRFYNTETGKCTMFSYGGCGGNENPFETIDCKACGA 73

```

Search completed: January 23, 2004, 10:27:16
 Job time : 31.2711 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 7.59859 Seconds
(without alignments)

513.676 Million cell updates/sec

Title: US-09-700-179a-22

Sequence: 1 MESSGALLLLGLTLTWELT.....CGGNANNFTIEEGSTCAA 83

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224	48.9	61	1	PO0991 vipera ammo
2	212	46.3	57	1	P20229 naja naja (
3	212	46.3	65	1	P25660 bungarus fa
4	209	45.6	57	1	PO0986 naja naja
5	207	45.2	57	1	PO0985 hemachatus
6	207	45.2	65	1	PO0982 vipera ammo
7	201	43.9	85	1	PO0989 bungarus mu
8	192	41.9	58	1	P2966 ophiophagus
9	189	41.3	62	1	P4541 eristocophi
10	186	40.6	60	1	PO0990 daboia ruse
11	184	40.2	62	1	P10280 anemonia su
12	184	40.2	85	1	PO0987 bungarus mu
13	178	38.9	57	1	PO0982 dendroaspis
14	178	38.9	57	1	PO0981 dendroaspis
15	172	37.6	55	1	P81902 bombyx mori
16	172	37.6	59	1	PO0984 dendroaspis
17	169	36.9	304	1	Q28864 macaca mula
18	167	36.5	58	1	P81547 anthopileura
19	167	36.5	300	1	P19713 oryctolagus
20	166	36.2	55	1	P11713 stictochactis
21	166	36.2	302	1	002445 rattus norv
22	165	36.0	55	1	P81139 stictochactis
23	165	36.0	110	1	P00993 catichactis
24	164	35.8	58	1	P00994 helix pomat
25	162	35.4	304	1	P10646 homo sapien
26	160	34.9	306	1	O54819 mus musculu
27	159.5	34.8	230	1	O5536 mus musculu
28	157	34.3	57	1	P19859 naja naja (
29	155	33.8	58	1	P81548 anthopileura
30	155	33.8	252	1	SPT22222222222222
31	153.5	33.4	500	1	P00990 dendroaspis
32	153	33.4	500	1	P00990 dendroaspis
33	150	32.8	60	1	PO0979 dendroaspis

34	150	32.8	235	1	TFP2_HUMAN	P48307 homo sapien
35	148.5	32.4	122	1	UPTI_PIG	Q29100 sus scrofa
36	147.5	32.2	100	1	BPT2_BOVIN	P04815 bos taurus
37	147	32.1	69	1	CRPT_BOVIN	P81162 boophyllus m
38	146.5	32.0	102	1	ELAC_TRIYU	Q29143 trichosurus
39	144.5	31.6	197	1	MCPI_MEICP	P82968 melitnaea c
40	143	31.2	507	1	SPT1_MOUSE	Q97097 mus musculu
41	141	30.8	60	1	IBPS_BOVIN	P00975 bos taurus
42	141	30.8	60	1	TXCA_DENAN	P81658 dendroaspis
43	141	30.8	763	1	APP2_HUMAN	O06481 homo sapien
44	140	30.6	57	1	IVB2_DENPO	PO0983 dendroaspis
45	140	30.6	351	1	TKD1_BOVIN	Q28201 bos taurus

ALIGNMENTS

RESULT 1	IVB1_VIPAA	STANDARD;	PRT;	61 AA.
ID	PO0991			
AC	PO0991			
DT	21-JUN-1986 (Rel. 01, Last sequence update)			
DT	21-JUN-1986 (Rel. 01, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Vipera ammodytes ammodytes (Western sand viper).			
OS	Vipera ammodytes ammodytes (Western sand viper).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Leiodontaria; Squamata; Scleroglossa; Serpentes; Colubroides;			
OC	Viperidae; Viperinae; Vipera.			
OX	NCBI_Taxid=8705;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=84053385; PubMed=6639951;			
RA	Ritonga A., Melom B., Gubensek F.;			
RT	"The primary structure of Vipera ammodytes venom trypsin inhibitor			
RT	I."			
RL	Biochim. Biophys. Acta 748:429-435(1983).			
CC	- FUNCTION: This protein inhibits trypsin and kallikrein.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	PIR; A01222; TIVITL.			
DR	HSSP; P31713; ISHP.			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam: PF00014; Kunitz_BPTI; 1.			
DR	ProDom: PD000222; Kunitz_BPTI; 1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
KW	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
DR	Serine protease inhibitor; Pyrrolidone carboxylic acid.			
FT	MOD_RES	1	1	
FT	DISULFID	7	57	
FT	DISULFID	16	40	
FT	DISULFID	32	53	
SQ	SEQUENCE	61 AA;	6865 MW;	FC8285F579FE3795 CRC64;
Query Match		48.9%;	Score 224;	DB 1; Length 61;
Best Local Similarity		62.7%;	Pred. No. 3.9e-16;	
Matches	37;	Conservative 10;	Mismatches 12;	Indels 0;
Qy	25	KDHPKFCFLPAFGSCGVPRFPYVNDHHQCLKFTYGGCGGNANFTIEEGSTCAA	83	
Db	1	QDHPKFCFLPAFGSCGVPRFPYVNDHHQCLKFTYGGCGGNANFTIEEGSTCAA	59	
RESULT 2	IVB1_NAJNA	STANDARD;	PRT;	57 AA.
ID	PO0229			
AC	PO0229			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom trypsin inhibitor.			

OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OC NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=9109304; PubMed=1702708;
 RA Shaifqat J., Beg O.U., Yin S.-J., Zaidi Z.H., Joernvall H.;
 RT "Primary structure and functional properties of cobra (Naja naja
 naja) venom Kunitz-type trypsin inhibitor.";
 RL Eur. J. Biochem. 194;337-341(1990).
 CC -1- FUNCTION: This protein inhibits trypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S13846; S13846.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6371 MW; AABPD7294ADC12A CRC64;

Query Match 46.3%; Score 212; DB 1; Length 57;
 Best Local Similarity 66.7%; Pred. No. 7.6e-17;
 Matches 36; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 28 PKFCELPATGSCCKGNVPRFYNNADHQCLEFYGGCGGNANPFXTIEGKSTC 81
 Db 2 PGFELPAAGLCKAHKPAFYNNDSHCQCFYGGCGGNANRRFTIDECHRTC 55

RESULT 3
 ID IVB1_BUNFA STANDARD; PRT; 65 AA.
 AC P25660;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitors IX and VIIIB.
 OS Bungarus fasciatus (Banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 OC NCBI_TaxID=8613;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=83160048; PubMed=6832893;
 RA Liu C.-S., Wu T.-C., Lo T.-B.;
 RT "Complete amino acid sequences of two protease inhibitors in the
 RT venom of Bungarus fasciatus.";
 RL Int. J. Pept. Protein Res. 21;209-215(1983).
 CC -1- FUNCTION: Inhibitor of chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P00980; IDTX.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

KM Serine protease inhibitor.
 FT DISULFID 7 57 BY SIMILARITY.
 FT DISULFID 16 40 BY SIMILARITY.
 FT DISULFID 32 53 BY SIMILARITY.
 FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
 FT VARIANT 63 65 MISSING (IN INHIBITOR VIIIB).
 SQ SEQUENCE 65 AA; 7294 MW; BA340749E194DB51 CRC64;

Query Match 46.3%; Score 212; DB 1; Length 65;
 Best Local Similarity 62.7%; Pred. No. 8.6e-17;
 Matches 37; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 25 KDHPCELPATGSCCKGNVPRFYNNADHQCLEFYGGCGGNANPFXTIEGKSTCA 83
 Db 1 KNRTFENLLPETERCNALIPAFYNNSHLHKQCFYGGCGGNANRRFTIDECHRTCA 59

RESULT 4
 ID IVB2_NAJNI STANDARD; PRT; 57 AA.
 AC P00985;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Naja naja (Cape cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OC NCBI_TaxID=8655;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Rhinophis corbra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them.";
 RL J. Biochem. 79;559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is probably similar to
 CC that of bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01217; TINJVC.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

Query Match 45.6%; Score 209; DB 1; Length 57;
 Best Local Similarity 66.7%; Pred. No. 1.6e-16;
 Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 28 PKFCELPATGSCCKGNVPRFYNNADHQCLEFYGGCGGNANPFXTIEGKSTC 81
 Db 2 PRFCELPATGELCKAIRSFHYNRAAQCLEFYGGCGGNANRRFTIDECHRTC 55

RESULT 5
 ID IVB2_HEMHA STANDARD; PRT; 57 AA.
 AC P00985;
 DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, last sequence update)
DR 28-FEB-2003 (Rel. 41, last annotation update)
DE Venom basic protease inhibitor II.
OS Hemichatus haemachatus (Ringhale) (Sepedon haemachatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC NCB1_TaxID=8626;
RN [1]
RP SEQUENCE.
RX MEDLINE=76237547; PubMed=950337;
RA Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;
RT "Snake venom proteinase inhibitors. III. Isolation of five
RT polypeptide inhibitors from the venoms of Hemichatus haemachatus
RT (Ringhale's cobra) and Naja naja (Cape cobra) and the complete amino
RT acid sequences of two of them."
RL J. Biochem. 79:559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is similar to that of
CC -1- bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR: A01216; TIRIVZ.
DR HSSP: P00981; IDTK.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI_1.
DR ProDom: PD000222; Kunitz_BPTI_1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7F2A CRC64;

Query Match 45.2%; Score 207; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 2, 7e-16;
Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 28 PRFCBPAETGSGKAVPRPYNADHHQCKFTYGGGGGANNFKTIEGKSTCA 81
DB 2 PRFCBPAETGSGKAVPRPYNADHHQCKFTYGGGGGANNFKTIEGKSTCA 55

RESULT 6
ID IYB3_VIPAA STANDARD; PRT; 65 AA.
AC P00952;
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).
OS Vipera ammodytes ammodytes (Western sand viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OC NCB1_TaxID=8705;
RN [1]
RP SEQUENCE.
RX MEDLINE=95031955; PubMed=7945237;
RA Ritonja A., Meloun B., Gubensek F.;
RT "The primary structure of Vipera ammodytes venom chymotrypsin
RT inhibitor."
RT Biochim. Biophys. Acta 746:138-145(1983).
CC -1- FUNCTION: This protein inhibits chymotrypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP: A01223; TIVIVC.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI_1.
DR ProDom: PD000222; Kunitz_BPTI_1.

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DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7CC57 CRC64;

Query Match 45.2%; Score 207; DB 1; Length 65;
Best Local Similarity 61.0%; Pred. No. 3, 1e-16;
Matches 36; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 25 KDRPCBPAETGSGKAVPRPYNADHHQCKFTYGGGGGANNFKTIEGKSTCA 83
DB 1 KDRPCBPAETGSGKAVPRPYNADHHQCKFTYGGGGGANNFKTIEGKSTCA 59

RESULT 7
ID IYB2_BUNMU STANDARD; PRT; 85 AA.
AC P00989; O42299; Q9PRV8; Q9PTA3;
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Beta bungarotoxin B2 chain precursor.
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCB1_TaxID=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=98359733; PubMed=9693106;
RA Wu P.-F., Wu S.N., Chang C.-C., Chang L.-S.;
RT "Cloning and functional expression of B chains of beta-bungarotoxins
RT from Bungarus multicinctus (Taiwan banded krait).";
RL Biochem. J. 334:87-92(1998).
RN [2]
RP SEQUENCE OF 1-82 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20363696; PubMed=10903499;
RA Wu P.-F., Chang L.-S.;
RT "Genetic structures of A chain and B chain of beta-bungarotoxin from
RT Taiwan banded krait (Bungarus multicinctus). A chain genes and B chain
RT genes do not share a common origin."
RL Eur. J. Biochem. 267:4668-4675(2000).
RN [3]
RP SEQUENCE OF 25-85.
RC TISSUE=Venom;
RX MEDLINE=82239269; PubMed=7096304;
RA Kondo K., Toda H., Narita K., Lee C.-Y.;
RT "Amino acid sequence of beta 2-bungarotoxin from Bungarus
RT multicinctus venom. The amino acid substitutions in the B chains."
RL J. Biochem. 91:1519-1530(1982).
RN [4]
RP SEQUENCE OF 25-63.
RX MEDLINE=95031955; PubMed=7945237;
RA Chu C.C., Chu S.T., Chen S.W., Chen Y.H.;
RT "The non-phospholipase A2 subunit of beta-bungarotoxin plays an
RT important role in the phospholipase A2-independent neurotoxic effect:
RT characterization of three isoforms with a common phospholipase A2
RT subunit."
RL Biochem. J. 303:171-176(1994).
RN [5]
RP REVIEW.
RX MEDLINE=20396379; PubMed=10936627;
RA Rowan E.G.;
RT "What does beta-bungarotoxin do at the neuromuscular junction?";
RL Toxicon 39:107-118(2001).
CC -1- FUNCTION: Beta-2 bungarotoxin is a presynaptic neurotoxin of the

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CC venom. The B chain is homologous to venom basic protease
 CC inhibitors but has no protease inhibitor activity and is non-
 CC toxic.
 CC -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
 CC The A chains have phospholipase A2 activity and the B chains show
 CC homology with the basic protease inhibitors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).

CC -----
 CC EMBL: Y12101; CAA72810.1; -
 CC EMBL: AJ251224; CAB62504.1; -
 CC PDB: 1BUN; 03-APR-96.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF00014; Kunitz_BPTI_1.
 CC ProDom: PD000222; Kunitz_BPTI_1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC Toxin: Neurotoxin; Presynaptic neurotoxin; Signal; 3D-structure.
 CC KMW: Toxin; Neurotoxin; Presynaptic neurotoxin; Signal; 3D-structure.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 85
 CC FT DOMAIN 31 81
 CC FT DISULFID 31 81
 CC FT DISULFID 40 64
 CC FT DISULFID 56 77
 CC FT DISULFID 79 79
 CC FT ACT_SITE 41 42
 CC FT CONFLICT 44 44
 CC FT CONFLICT 65 70
 CC FT CONFLICT 82 83
 CC FT SEQUENCE 85 AA; 9568 MW; FE95A59AF92BF2MA CRC64;
 CC Query Match 43.9%; Score 201; DB 1; Length 85;
 CC Best Local Similarity 58.1%; Pred. No. 1.8e-15;
 CC Matches 43; Conservative 8; Mismatches 21; Indels 2; Gaps 2;

QY 1 MSSGGLLLGLLTWEVLTPEVS-KDHPKCELPAGTSGCKGNPRRYNADHHQCLKF 59
 DB 1 MSSGGLLLGLLTWEVLTPEVS-KDHPKCELPAGTSGCKGNPRRYNADHHQCLKF 59
 QY 60 IYGGCGGNANPKT 73
 DB 60 IYGGCGGNANPKT 73
 DB 60 RYGGCGNGNHPKS 73

RESULT 8
 IVBC_OPHNA STANDARD; PRT; 58 AA.
 AC P82966;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom chymotrypsin inhibitor.
 OS Ophiophagus hannah (King cobra) (Naja hannah).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Elapidae; Elapinae; Ophiophagus.
 CC NCBI_Taxid=8665;
 CC (1)
 RN
 RP SEQUENCE.
 RC TISSUE=Venom gland;
 RX MEDLINE=21248396; PubMed=11350064;
 RA Chang L.-S., Chung C., Huang H.-B., Lin S.-R.;
 RT "Purification and characterization of a chymotrypsin inhibitor from

RT the venom of Ophiophagus hannah (King Cobra).";
 RL Biochem. Biophys. Res. Commun. 283:862-867(2001).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC HSSP: P00981; IDTK.
 CC DR GO: GO:0005576; C:extracellular; NAS.
 CC DR GO: GO:0004867; F:serine protease inhibitor activity; IDA.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC DR Pfam: PF00014; Kunitz_BPTI_1.
 CC DR PRINTS: PR00759; BASICTPASE.
 CC DR ProDom: PD000222; Kunitz_BPTI_1.
 CC DR SMART: SM00131; KU; 1.
 CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC KW Serine protease inhibitor.
 CC FT DISULFID 6 56
 CC FT DISULFID 15 39
 CC FT DISULFID 31 52
 CC FT ACT_SITE 16 17
 CC FT SEQUENCE 58 AA; 6499 MW; 3EB44C85F0843D8A CRC64;
 CC Query Match 41.9%; Score 192; DB 1; Length 58;
 CC Best Local Similarity 63.0%; Pred. No. 1.2e-14;
 CC Matches 34; Conservative 2; Mismatches 18; Indels 0; Gaps 0;

QY 28 PKFCELPAGTSGCKGNPRRYNADHHQCLKFIIYGGCGGNANPKTIEGKSTC 81
 DB 3 PKFCELPAGTSGCKGNPRRYNADHHQCLKFIIYGGCGGNANPKTIEGKSTC 81

RESULT 9
 IVBT_ERIMA STANDARD; PRT; 62 AA.
 AC P24541;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis macmahoni (Leaf-nosed viper).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC OC Viperidae; Viperinae; Eristocophis.
 CC NCBI_Taxid=8702;
 CC (1)
 RN
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=92077130; PubMed=1743283;
 RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 RT from leaf-nosed viper venom.";
 RL FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC DR PIR: S19327; S19327.
 CC DR HSSP: P00981; IDTK.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC DR Pfam: PF00014; Kunitz_BPTI_1.
 CC DR PRINTS: PR00759; BASICTPASE.
 CC DR ProDom: PD000222; Kunitz_BPTI_1.
 CC DR SMART: SM00131; KU; 1.
 CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC KW Serine protease inhibitor.
 CC FT DISULFID 2 52
 CC FT DISULFID 11 35
 CC FT DISULFID 27 48
 CC FT ACT_SITE 12 13
 CC FT SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;
 CC Query Match 41.3%; Score 189; DB 1; Length 62;
 CC Best Local Similarity 59.3%; Pred. No. 2.8e-14;

Matches 32; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 30 FCELPATGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTCA 83
DB 1 FCTLPDPGCKAHIFRYNNPASNCKNFYGGCGGNANFKTIEGKSTCA 54

RESULT 10
ID IVB2_DABRU STANDARD; PRT; 60 AA.
AC P00930;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II (RVV-II).
OS Dabola russelli siamensis (Siamese Russell's viper) (Vipera russelli siamensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Dabola.
NCBI_TaxID=8708;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=75060360; PubMed=4436285;
RA Takahashi H., Iwanaga S., Kitagawa T., Hokama Y., Suzuki T.;
RT "Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II isolated from the venom of Russell's viper (Vipera russelli)."
RT J. Biochem. 76:721-733(1974).
CC -1- FUNCTION: This inhibitor has activity similar to bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P10646; IADZ.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; Ku; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
FT ACT_SITE 17 18
SQ SEQUENCE 60 AA; 6850 MW; 5A7DCB9554CE6A2 CRC64;

Query Match 40.6%; Score 186; DB 1; Length 60;
Best Local Similarity 53.6%; Pred. No. 5.9e-14;
Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 26 DHPKCELPATGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 81
DB 2 DRPTPCULAPESGCRGHLIRIYNLSNCKVFYGGCGGNANFKTIEGKSTC 57

RESULT 11
ID IP52_ANESU STANDARD; PRT; 62 AA.
AC P10250;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor 5 II (SAS II).
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymphaeae; Actiniidae; Anemonia.
NCBI_TaxID=6108;
RN [1]
RP SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone

RT Anemonia sulcata.";
RL Mech. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide from the sea anemone Metridium senile."
RL Naturwissenschaften 74:395-396(1987).
CC -1- FUNCTION: INHIBITOR OF KALLIKREIN.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S07451; S07451.
DR HSSP; P31713; ISHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASR.
DR PRODom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; Ku; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55
FT DISULFID 14 38
FT DISULFID 30 51
FT ACT_SITE 15 16
FT VARIANT 13 13
FT VARIANT 16 16
FT VARIANT 17 17
FT VARIANT 25 25
FT VARIANT 28 28
FT VARIANT 39 39
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 40.2%; Score 184; DB 1; Length 62;
Best Local Similarity 58.8%; Pred. No. 1e-13;
Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 31 CELPAPATGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 81
DB 5 CELPKVGPGRARPRFYNNSSRCRCKFYGGCGGNANFKTIEGKSTC 55

RESULT 12
ID IVB1_BUNMU STANDARD; PRT; 85 AA.
AC P00987; O42298; P00988;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta bungarotoxin B1 chain, major component precursor.
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Elapidae; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Bungarinae; Bungarus.
NCBI_TaxID=6616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=98359733; PubMed=9693106;
RA Wu P.-F., Wu S.N., Chang C.-C., Chang L.-S.;
RT "Cloning and functional expression of B chains of beta-bungarotoxins from Bungarus multicinctus (Taiwan banded krait)."
RL Biochem. J. 334:87-92(1998).
RN [2]
RP SEQUENCE OF 25-85.
RC TISSUE=Venom;
RX MEDLINE=78109400; PubMed=624701;
RA Kondo K., Narita K., Lee C.-Y.;
RT "Amino acid sequences of the two polypeptide chains in beta-bungarotoxin from the venom of Bungarus multicinctus.";
RL J. Biochem. 83:101-115(1978).
RN [3]
RP MUTAGENESIS OF CYS-32.
RX MEDLINE=21589307; PubMed=11732693;

RA Wu P.-F., Chang L.-S.;
 RT "Expression of A chain and B chain of beta-bungarotoxin from Taiwan
 RT banded krait: the functional implication of the interchain disulfide
 RT bond between A chain and B chain.";
 RL J. Protein Chem. 20:413-421(2001).
 RN [4]
 RP REVIEW.
 RX MEDLINE=20396379; PubMed=10936627;
 RA Rowan B.G.;
 RT "What does beta-bungarotoxin do at the neuromuscular junction?";
 RL Toxicon 33:107-118(2001).
 CC -1- FUNCTION: Beta-1 bungarotoxin is a presynaptic neurotoxin of the
 CC venom. The B chain is homologous to venom basic protease
 CC inhibitors but has no protease inhibitor activity and is non-
 CC toxic.
 CC -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
 CC The A chains have phospholipase A2 activity and the B chains show
 CC homology with the basic protease inhibitors.
 CC -1- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC DR HSBP; Y12100; CAA72809.1; -
 CC DR HSBP; P00981; IDTK.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC DR Pfam: PF00014; Kunitz_BPTI_1.
 CC DR ProDom: PD000222; Kunitz_BPTI; 1.
 CC DR SMART; SM00131; KU; 1.
 CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 CC KW Toxin; Neurotoxin; Presynaptic neurotoxin; Signal.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 85
 CC FT DOMAIN 31 81
 CC FT DISULFID 31 81
 CC FT DISULFID 40 64
 CC FT DISULFID 56 77
 CC FT DISULFID 79 79
 CC FT ACT_SITE 41 42
 CC FT MUTAGEN 79 79
 CC FT CONFLICT 45 45
 CC FT CONFLICT 65 70
 CC FT SEQUENCE 85 AA; 9571 MW; A1E3D452AE67DE5C CRC64;
 SO
 Query Match 40.2%; Score 184; DB 1; Length 85;
 Best Local Similarity 55.4%; Pred. No. 1, 4e-13;
 Matches 41; Conservative 7; Mismatches 24; Indels 2; Gaps 2;
 QY 1 MSSGGLLLGLTTEVLTTPVSKDHPFCELPATGSCCKGNVPP-FTYNDHQCCKLF 59
 DB 1 MSSGGLLLGLTTCABLLPVSSRRHRDCDKPDKGNC-GPVRAFYDRLKCKCKAF 59
 QY 60 IYGGGGGANNPKT 73
 DB 60 QYRGCKGNANPKT 73
 RESULT 13
 ID IVBK DENAN STANDARD; PRT; 57 AA.
 AC P00982;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Venom basic protease inhibitor K (Dendrotoxin delta-DaTx) (Toxin
 DB C13S1C3).
 OS Dendroaspis angusticeps (Eastern green mamba).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8618;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81045446; PubMed=7429422;
 RA Joubert F.U., Taljard N.;
 RT "Snake venoms. The amino acid sequences of two proteinase inhibitor
 RT homologues from Dendroaspis angusticeps venom.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:661-674(1980).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=88318591; PubMed=2457792;
 RA Benishin C.G., Sorensen R.G., Brown W.E., Krueger B.K.,
 RA Blaustein M.P.;
 RT "Four polypeptide components of green mamba venom selectively block
 RT certain potassium channels in rat brain synaptosomes";
 RL Mol. Pharmacol. 34:152-159(1988).
 CC -1- FUNCTION: This protease inhibitor homolog has very low toxicity.
 CC It blocks voltage-gated potassium channels and facilitate
 CC neurotransmitter release.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: LD(50) is 15 mg/kg by intravenous injection.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC PIR; A51691; TIEPVA.
 CC DR HSBP; P00981; IDTK.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC DR Pfam: PF00014; Kunitz_BPTI_1.
 CC DR ProDom: PD000222; Kunitz_BPTI; 1.
 CC DR SMART; SM00131; KU; 1.
 CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 CC KW Serine protease inhibitor; Toxin; Neurotoxin;
 KW Potassium channel inhibitor.
 CC FT DISULFID 5 55
 CC FT DISULFID 14 38
 CC FT DISULFID 30 51
 CC FT ACT_SITE 15 16
 CC FT SEQUENCE 57 AA; 6574 MW; A4070CBB14DE93 CRC64;
 SO
 Query Match 38.9%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 4, 3e-13;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;
 QY 29 KFCCLPATGSCCKGNVPPFTYNDHQCCKLFYGGGGGANNPKTIEGKSTC 81
 DB 3 KCKCPVRRGPKKKKIPSYFKMKAKQCLPFYSGGGGANNPKTIEGKRTC 55
 RESULT 14
 ID IVBK DENPO STANDARD; PRT; 57 AA.
 AC P00981;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Venom basic protease inhibitor K (Dendrotoxin K).
 OS Dendroaspis polyplepis polyplepis (Black mamba).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8620;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77158069; PubMed=857902;
 RA Strydom D.O.;
 RT "Snake venom toxins. The amino acid sequence of toxin Vi2, a
 RT homologue of pancreatic trypsin inhibitor, from Dendroaspis polyplepis

RT poly(lep) (black mamba) venom.";
 RL Biochim. Biophys. Acta 491:361-369(1977).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94076347; PubMed=8254670;
 RA Bernik K.D., Guentert P., Wuehrlich K.;
 RT "Nuclear magnetic resonance solution structure of dendrotoxin K from
 the venom of Dendroaspis polyleps polyleps.";
 RL J. Mol. Biol. 234:735-750(1993)
 CC -1- FUNCTION: This protein is much less toxic to mice than is whole
 venom. It inhibits trypsin slightly, but chymotrypsin not at all.
 CC It is a highly selective blocker of voltage-gated potassium
 channels.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: LD(50) IS 30 MG/KG BY INTRAVENOUS INJECTION.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PDB, 1DK; 31-JAN-94.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; toxin; Neurotoxin; Ionic channel inhibitor;
 KW 3D-structure; Potassium channel inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 FT HELIX 3 6
 FT STRAND 18 24
 FT TURN 25 28
 FT STRAND 29 35
 FT STRAND 45 45
 FT HELIX 48 55
 SQ SEQUENCE 57 AA; 6566 MW; C30818FB3C41CB87 CRC64;
 Query Match 38.9%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 4,3e-13;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;
 QY 29 KFCLEPAETGSCGNVRFYTNADHQCLEKRYGCGGANNANFKTIEGKSTC 81
 DB 3 KYCKLPLRIQPCPKRKIPSPFYKWKAKQCLPFDYSGCGGANNANFKTIEGKSTC 55
 RESULT 15
 CSTI_BOMMO
 ID ID CSTI_BOMMO STANDARD; PRT; 55 AA.
 AC P81902;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 OX [1]
 RP SEQUENCE AND CHARACTERIZATION.
 RC STRAIN=Asahi;
 RX MEDLINE=99115431; PubMed=9914483;
 RA Kurioka A., Yamazaki M., Hirano H.;
 RT "Primary structure and possible functions of a trypsin inhibitor of
 Bombyx mori.";
 RL Eur. J. Biochem. 259:120-126(1999).
 CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
 activity by forming a low-dissociation complex with trypsin. May
 play an important part in regulating proteolytic activity in the
 silk gland or protecting silk proteins from degradation during
 histolysis.
 CC -1- SUBUNIT: Monomer.

CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
 CC gland.
 CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
 CC middle silk glands during the final stage of larval growth with
 CC highest expression before the onset of spinning.
 CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
 CC -1- MISCELLANEOUS: Has an isoelectric point of 4.3.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR HSPSP; P31713; 1SHP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICPTASB.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Developmental protein; Serine protease inhibitor.
 FT DISULFID 54 54 BY SIMILARITY.
 FT DISULFID 13 37 BY SIMILARITY.
 FT DISULFID 29 50 BY SIMILARITY.
 FT ACT_SITE 14 15 REACTIVE BOND (TRYPSIN) (BY
 SIMILARITY).
 SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2BB6E59 CRC64;
 Query Match 37.6%; Score 172; DB 1; Length 55;
 Best Local Similarity 54.9%; Pred. No. 1.9e-12;
 Matches 28; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 31 CELPAPETGSCGNVRFYTNADHQCLEKRYGCGGANNANFKTIEGKSTC 81
 DB 4 CLPPIKTPCKGSPPRAYDSSBDKCVFHYGGGANNANFKTIEGKSTC 54

Search completed: January 23, 2004, 10:25:15
 Job time : 7.59859 secs

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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:23 ; Search time 12.8592 Seconds
(without alignments)
620.725 Million cell updates/sec

Title: US-09-700-179a-22

Sequence: 1 MSGGILLILGLTWEVL.....CGGNANFKTIEBKSTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	54.1	79	1	TIEPVK K+ channel blocker
2	224	48.9	61	1	TIVTIL venom basic protei
3	212	46.3	57	2	S13846 venom animal Kunitt
4	209	45.6	57	1	TINIVC venom basic protei
5	207	45.2	57	1	TIRIVZ venom basic protei
6	207	45.2	65	1	TIVIVC venom basic protei
7	202	44.1	62	2	A44180 calcatoxin serine
8	189	41.3	62	2	S19327 venom basic protei
9	186	40.6	60	2	TIVRZV venom basic protei
10	184	40.2	62	2	S07451 proteinase inhibit
11	178	38.9	57	1	TIBPVA venom basic protei
12	174	38.0	57	2	A59204 basic proteinase i
13	172	37.6	57	2	B59399 short epsilon-dend
14	172	37.6	59	1	TIBEPD venom basic protei
15	172	37.6	59	2	A59399 long epsilon-dend
16	169	36.9	304	1	JC2264 tissue factor path
17	167.5	36.6	299	2	I46937 tissue factor path
18	167	36.5	300	2	S12143 lipoprotein-asept
19	166	36.2	55	2	S30332 proteinase inhibit
20	166	36.0	110	1	TITRCK tissue factor path
21	165	36.0	110	1	TITRCK tissue factor path
22	164	35.8	58	1	TTHARK tissue factor path
23	162	35.4	304	1	TTHARK tissue factor path
24	158	34.5	396	2	S53325 venom animal Kunitt
25	157	34.3	57	2	S12957 protein C37C3.6a
26	154	33.6	1558	2	C89114 hypothetical prote
27	154	33.6	2167	2	T34335 basic proteinase i
28	153.5	33.5	100	1	TIBO venom basic protei
29	153	33.4	59	1	VIEPIA venom basic protei

30	153	33.4	2225	2	T26063 hypothetical prote
31	152	33.2	249	2	T32060 hypothetical prote
32	150	32.8	60	1	TIEPVI venom basic protei
33	150	32.8	235	2	A54951 tissue factor path
34	148.5	32.4	122	1	A55115 uterine plasmin/tr
35	147.5	32.2	100	1	TIBOSP spleen basic prote
36	146.5	32.0	102	2	S69288 early laccation pr
37	144	31.4	111	2	S41082 amyloid precursor
38	144	31.4	805	2	T34212 hypothetical prote
39	143	31.2	59	2	S00371 isoprotein G1 -
40	143	31.2	747	2	JH0773 Alzheimer's diseas
41	142	31.0	1965	2	T33216 hypothetical prote
42	141	30.8	58	1	S10063 isoprotein G2 -
43	141	30.8	60	1	TIBOR serum basic protei
44	141	30.8	60	2	A36989 calcitriol - eas
45	141	30.8	751	2	A49974 beta-amyloid precu

ALIGNMENTS

RESULT 1

K+ channel blocker dendrotoxin K - black mamba
C/Species: Dendroaspis polylepsis polylepsis (black mamba)
C/Date: 30-Nov-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C/Accession: A49291; A01213
R/Smith, L.A.; Lafaye, P.J.; Lapenotiere, H.F.; Spain, T.; Dolly, J.O.
Biochemistry 32, 5692-5697, 1993
A/Title: Cloning and functional expression of dendrotoxin K from black mamba, a K+ char
A/Reference number: A49291; MUID:93277850; PMID:8504088
A/Accession: A49291
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-79 <SM>
A/Cross-references: GB:S61886; NID:G385317; PID:AA826998.1; PID:G385318
A/Note: sequence extracted from NCBI backbone (NCBI:133053, NCBI:P:133054)
A/Note: the source is designated as Dendroaspis polylepsis
R/Strydom, D.J.
Biochim. Biophys. Acta 491, 361-369, 1997
A/Title: Snake venom toxins. The amino acid sequence of toxin Vi2, a homologue of panc
A/Reference number: A90617; MUID:77158069; PMID:857902
A/Accession: A01213
A/Molecule type: protein
A/Residues: 23-79 <STR>
C/Comment: This protein is much less toxic to mice than is whole venom. It inhibits try
C/Suprafamily: basic proteinase inhibitor; animal Kunitt-type proteinase inhibitor homoc
C/Keywords: serine proteinase inhibitor; venom
F:27-77/Domain: animal Kunitt-type proteinase inhibitor homology <BPI>
F:27-77,36-60,52-73/Disulfide bonds: #status predicted

Query Match 54.1%; Score 248; DB 1; Length 79;
Best Local Similarity 62.0%; Pred. No. 1.4e-20;
Matches 49; Conservative 4; Mismatches 24; Indels 2; Gaps 1;

Qy	3	SGGILLILGLTWEVLTPVSSKHPRCEPAETGSCGVNPPRYNADHQCIFYG	62
Db	1	SGHLLILGLTMAELTPVSGA-AKYCKPLRIIGPKRKIPSTYRKAKKQCLPDIS	58
Qy	63	CGCGNANFKTIEBKSTC	81
Db	59	CGCGNANFKTIEBKSTC	77

RESULT 2

venom basic proteinase inhibitor I - western sand viper
N/Alternate names: venom trypsin inhibitor I
C/Species: Vipera ammodytes ammodytes (western sand viper)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996
C/Accession: A01222
R/Ritconja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 748, 429-435, 1983

RESULT 5

TIRIY2

venom basic proteinase inhibitor II - ringhals

C:Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01216

R:Okama, Y.; Iwanaga, S.; Tateuchi, T.; Suzuki, T.

J. Biochem. 79, 559-578, 1976

A:Title: Snake venom proteinase inhibitor. III. Isolation of five polypeptide inhibitors of acid sequences of two of them.

A:Reference number: A91942; MUID:76237547; PMID:950337

A:Accession: A01216

A:Molecule type: Protein

A:Residues: 1-57 <HOK>

C:Comment: The activity of this inhibitor is similar to that of bovine basic proteinase C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor hom C:Keywords: serine proteinase inhibitor; venom

F:5-55/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 45.2%; Score 207; DB 1; Length 57;

Best Local Similarity 66.7%; Pred. No. 3.7e-16;

Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

RESULT 6

TIVIC

venom basic proteinase inhibitor III - sand viper

N:Alternate names: venom chymotrypsin inhibitor

C:Species: Vipera ammodytes (sand viper)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Aug-1996

C:Accession: A01223

R:Rittonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 746, 138-145, 1983

A:Title: The primary structure of Vipera ammodytes venom chymotrypsin inhibitor.

A:Reference number: A01223

A:Accession: A01223

A:Molecule type: Protein

A:Residues: 1-65 <RT>

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor hom C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status predicted

F:17/Inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 45.2%; Score 207; DB 1; Length 65;

Best Local Similarity 61.0%; Pred. No. 4.2e-16;

Matches 36; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

RESULT 7

A44180

calicotoxin serine proteinase inhibitor component - Australian taipan

C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)

C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C:Accession: A44180

R:Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, U.; Zamudio, F.Z.; Gurrola, A.;

toxin 30, 1343-1364, 1992

A:Title: Isolation and physiological characterization of calicotoxin, a complex toxin w

A:Accession: A44180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Experimental source: subsp. scutellatus, venom
A>Note: Sequence extracted from NCBI backbone (NCBIP:122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:1-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 44.1%; Score 202; DB 2; Length 62;
Best Local Similarity 61.4%; Pred. No. 1.4e-15;
Matches 35; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

25 KDHPKCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 81
1 KDHPKCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 57

RESULT 8
S19327
venom basic proteinase inhibitor - leaf-nosed viper
N:Alternate names: trypsin inhibitor (Kunitz-type)
C:Species: Eristocophis macdonaldi (leaf-nosed viper)
C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C:Accession: S19327
R:Submitted: A.R.; Zaidi, Z.H.; Joernvall, H.
PDBS Lett. 294, 141-143, 1991
A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from leaf-
A:Reference number: S19327; PMID:9207130; PMID:1743283
A:Accession: S19327
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62 <STD>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 41.3%; Score 189; DB 2; Length 62;
Best Local Similarity 59.3%; Pred. No. 4e-14;
Matches 32; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

30 FCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTCA 83
1 FCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTCA 54

RESULT 9
T19V2
venom basic proteinase inhibitor II - Russell's viper
C:Species: Vipera russelli (Russell's viper)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01221
R:Takahashi, H.; Iwanaga, S.; Kitagawa, T.; Hokama, Y.; Suzuki, T.
J. Biochem. 76, 721-733, 1974
A:Title: Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II isol
A:Reference number: A01221; PMID:75060360; PMID:4436285
A:Accession: A01221
A:Molecule type: protein
A:Residues: 1-60 <TK>
C:Comment: This inhibitor has activity similar to that of bovine basic protease inhibi
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 40.6%; Score 186; DB 1; Length 60;
Best Local Similarity 53.6%; Pred. No. 8.4e-14;
Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

26 DHPKCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 81
2 DHPKCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 57

RESULT 10
S07451
proteinase inhibitor 5.II - snake-locks sea anemone
C:Species: Anemonia sulcata (snake-locks sea anemone)
C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: S07451; B27222
R:Wunderer, G.; Machleidt, W.; Fritzt, H.
Meth. Enzymol. 80, 816-820, 1991
A:Title: The broad-specificity proteinase inhibitor 5.II from the sea anemone Anemonia
A:Reference number: S07451
A:Accession: S07451
A:Molecule type: protein
A:Residues: 1-59 <MIN>
A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R:Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A:Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus der
A:Reference number: A94700
A:Accession: B27222
A:Molecule type: protein
A:Residues: 1-38, 'R', '40', 'B', '42', 'BB', '45-48', 'ZZ', '51', 'Z', '53-62 <KRE>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homo
C:Keywords: serine proteinase inhibitor
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 40.2%; Score 184; DB 2; Length 62;
Best Local Similarity 58.8%; Pred. No. 1.4e-13;
Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

31 CELPAPFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 81
5 CELPAPFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 55

RESULT 11
T19PVA
venom basic proteinase inhibitor K - eastern green mamba
N:Alternate names: dendrotoxin delta-Dark
C:Species: Dendroaspis angusticeps (eastern green mamba)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C:Accession: A91691; C32508; A01213
R:Joubert, P.J.; Taljaard, N.
Hoppe-seyler's Z. Physiol. Chem. 361, 661-674, 1980
A:Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroasp
A:Reference number: A91691; PMID:81045446; PMID:7429422
A:Accession: A91691
A:Molecule type: protein
A:Residues: 1-57 <10U>
R:Benjamin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.
Mol. Pharmacol. 34, 152-159, 1988
A:Title: Four polypeptide components of green mamba venom selectively block certain pot.
A:Reference number: A93137; PMID:88318591; PMID:2457792
A:Accession: C32508
A:Molecule type: protein
A:Residues: 1-21 <BN>
A:Note: the amino acid composition of the inhibitor is identical with that predicted fr
C:Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological fu
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homo
C:Keywords: venom
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 38.9%; Score 178; DB 1; Length 57;
Best Local Similarity 58.5%; Pred. No. 6.2e-13;
Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

29 KCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 81
3 KCELPALFATGSCGNVPRFYVADHQCCKFYGGCGGANNFTIEBKGSTC 55

RESULT 12

A59204 basic proteinase inhibitor - great pond snail

N/Alternate names: trypsin inhibitor

C/Species: Lymnaea stagnalis (great pond snail)

C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 17-Mar-2000

C/Accession: A59204

R/Tagline: G

submitted to the Protein Sequence Database, March 2000

A/Description: Lymnaea trypsin inhibitor.

A/Reference number: A59204

A/Accession: A59204

A/Molecule type: protein

A/Residues: 1-57 <NAG>

A/Experimental source: albumen gland

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: glycoprotein; serine proteinase inhibitor

F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/5-55/14-38/30-51/Disulfide bonds: #status predicted

F/15/Inhibitory site: Lys (trypsin) #status predicted

F/24/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 38.0%; Score 174; DB 2; Length 57;

Best Local Similarity 54.9%; Pred. No. 1.7e-12;

Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

OY 31 CELPAETGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTTIEGKSTC 81

DB 5 CSIPSESGPCCKGNFLRYHNSSTNACDFVGGCGGANNPDDIDCKRAC 55

RESULT 13

B59399 short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps

C/Species: Dendroaspis angusticeps

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C/Accession: B59399

R/Signle: R.; Hackert, M.; Aird, S.D.

Toxicon 40; 297-308, 2002

A/Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis

A/Reference number: A59399

A/Accession: B59399

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <AIR>

A/Note: trypsin inhibitor; K+ channel antagonist

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F/5-55/Disulfide bonds: #status experimental

F/14-36/Disulfide bonds: #status experimental

F/30-51/Disulfide bonds: #status experimental

Query Match 37.6%; Score 172; DB 2; Length 57;

Best Local Similarity 54.5%; Pred. No. 2.9e-12;

Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 27 HPKCELPATGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTTIEGKSTC 81

DB 1 HRTFCKLPABPGPKASIPAFYTNMAKCOLFHYGGCGGANNRSTIEKCRHAC 55

RESULT 14

TIBPBD venom basic proteinase inhibitor B - black mamba

C/Species: Dendroaspis polyolepis polyolepis (black mamba)

C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C/Accession: A01215

R/Joubert, F.J.; Stridom, D.J.

Eur. J. Biochem. 87, 191-198, 1978

A/Title: Snake venoms: the amino-acid sequence of trypsin inhibitor B of Dendroaspis pol

A/Reference number: A01215; MUID:7821615; PMID:66868

A/Accession: A01215

A/Molecule type: protein

A/Residues: 1-59 <JOU>

A/Note: this protein inhibits trypsin and binds transition metal ions such as copper at

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/7-57/16-40/32-53/Disulfide bonds: #status predicted

Query Match 37.6%; Score 172; DB 1; Length 59;

Best Local Similarity 54.5%; Pred. No. 3e-12;

Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 27 HPKCELPATGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTTIEGKSTC 81

DB 3 HRTFCKLPABPGPKASIPAFYTNMAKCOLFHYGGCGGANNRSTIEKCRHAC 57

RESULT 15

A59399 long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps

C/Species: Dendroaspis angusticeps

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C/Accession: A59399

R/Signle: R.; Hackert, M.; Aird, S.D.

Toxicon 40; 297-308, 2002

A/Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis

A/Reference number: A59399

A/Accession: A59399

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-59 <AIR>

A/Note: trypsin inhibitor; K+ channel antagonist

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F/7-57/Disulfide bonds: #status experimental

F/15-40/Disulfide bonds: #status experimental

F/32-53/Disulfide bonds: #status experimental

Query Match 37.6%; Score 172; DB 2; Length 59;

Best Local Similarity 54.5%; Pred. No. 3e-12;

Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 27 HPKCELPATGSCGKGVPRFYTNADHQCCKFYGGCGGANNKTTIEGKSTC 81

DB 3 HRTFCKLPABPGPKASIPAFYTNMAKCOLFHYGGCGGANNRSTIEKCRHAC 57

Search completed: January 23, 2004, 10:28:11

Job time : 12.8592 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 40.0387 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179A-22

Perfect score: 458

Sequence: 1 MSGGLLLGLLTLMEVLT.....CGGNANNKTIIECKSTCAA 83

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq_19Jun03:*

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	458	100.0	83 21	AAV15148
2	372	81.2	83 21	AAV15147
3	342	74.7	59 21	AAV15141
4	341	74.5	83 21	AAV15145
5	333	72.7	83 21	AAV15146
6	317	69.2	83 21	AAV15149
7	308	67.2	83 21	AAV15150
8	256	55.9	59 21	AAV15140
9	239	52.2	60 21	AAV15151

10	225	49.1	59	21	AAV15138
11	218	47.6	60	21	AAV15153
12	217	47.4	59	21	AAV15139
13	211	46.1	58	17	AAV15146
14	201	43.9	59	21	AAV15142
15	193	42.1	60	21	AAV15154
16	192	41.9	59	21	AAV15143
17	178	38.9	57	15	AAV15255
18	172	37.6	58	16	AAV15191
19	170	37.1	58	16	AAV178542
20	169	36.9	304	14	AAV142309
21	168	36.7	58	16	AAV141915
22	166	36.2	58	16	AAV141892
23	166	36.2	58	17	AAV141917
24	166	36.2	302	14	AAV15001
25	166	36.2	302	17	AAV188513
26	165	36.0	58	17	AAV189195
27	165	36.0	83	17	AAV189218
28	164	35.8	58	14	AAV189800
29	164	35.8	111	14	AAV189807
30	163	35.6	161	17	AAV180017
31	163	35.6	291	24	AAV1848476
32	163	35.6	291	24	AAV1848478
33	162	35.4	58	17	AAV189194
34	162	35.4	160	13	AAV183800
35	162	35.4	183	12	AAV11146
36	162	35.4	225	22	AAV102971
37	162	35.4	286	12	AAV11169
38	162	35.4	261	12	AAV11171
39	162	35.4	262	12	AAV11172
40	162	35.4	265	12	AAV11170
41	162	35.4	276	17	AAV12265
42	162	35.4	276	17	AAV12012
43	162	35.4	276	18	AAV10311
44	162	35.4	276	19	AAV15155
45	162	35.4	276	24	AAV07724

ALIGNMENTS

RESULT 1	
AAV15148	AAV15148 standard; Protein: 83 AA.
XX	
AC	AAV15148;
XX	
DT	07-FEB-2000 (first entry)
XX	
DE	Proform of Txln 4 protein.
XX	
XX	Textillinin proform; Txln 4; plasmin inhibitor; single stage inhibitor;
KW	Australian brown snake; conserved cysteine residue; stability; control;
KW	haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
KW	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW	reduced propensity; chromoblasts.
XX	
OS	Pseudonaja textilis textilis.
XX	
PH	Key
FT	Peptide
FT	Protein
FT	Location/Qualifiers
FT	1..24
FT	/label= Leader peptide
FT	25..83
FT	/label= Txln-4 protein
FT	/note= "Textillinin-4"
XX	
PN	W0958569-A1.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WC-AU00343.
XX	

Txln 1 Plasmin inh
Plasmin inhibitor
Txln 2 Plasmin inh
Aprotinin-like Kun
Txln 5 Plasmin inh
Plasmin inhibitor
Txln 6 Plasmin inh
Protease-inhibitor
Kallikrein inhibit
Human LACT-K2 deri
LACT gene product.
LACT Kunitz domain
Kallikrein inhibit
Genetically engine
LACT. Rattus ratt
Lipoprotein-associ
Genetically engine
Human aprotinin-11
Kunitz-type protea
Synthetic yeast le
TPPI chimeric prot
Human Tifapinix.
Human Tifapinix-A5
Genetically engine
LACT fragment 1 -
Ser-(Glu15-Thr161)
Angiotensin conver
Ser(Asp1-Thr255)-E
Ser-(Asp1-Glu245)-
Ser-(Asp1-Ser248)-
Ser-(Asp1-Ile253)-
TPPI mucin. Lv836
Recombinant non-gl
Human tissue facto
Human tissue facto

PR 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI/) LAVIN M P.
 PA (GAF/) GAFNEY P J.
 PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 DR WPI; 2000-039073/03.
 DR N-PSDB; AAZ20927.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PS Claim 40d; Page 72; 112pp; English.
 CC The present sequence is the proform of the Textillinin protein, Txln 4,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 SO Sequence 83 AA;
 Query Match 100.0%; Score 458; DB 21; Length 83;
 Best Local Similarity 100.0%; Pred. No. 4e-48;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSGGILLLLGLLTMEVLTVPVSSKDHPCFCLPATGSCCKGNVPRFYNNADHQCCKFI 60
 DB 1 MSSGGILLLLGLLTMEVLTVPVSSKDHPCFCLPATGSCCKGNVPRFYNNADHQCCKFI 60
 QY 61 YGGCGGANNFRTIEGKSTCA 83
 DB 61 YGGCGGANNFRTIEGKSTCA 83
 RESULT 2
 ID AAY15147 standard; Protein; 83 AA.
 AC AAY15147;
 DT 07-FEB-2000 (first entry)
 DE Proform of Txln 3 protein.
 XX Textillinin proform; Txln 3; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 OS Pseudonaja textilis textilis.
 XX Key Location/Qualifiers
 FM 1..24
 FT /label= leader_peptide
 FT 25..83
 FT /label= Txln-3_protein
 FT /note= "Textillinin-3"
 PN MO9958569-A1.

XX 18-NOV-1999.
 PD 99WO-AU00343.
 XX 07-MAY-1999; 99WO-AU00343.
 PE 11-MAY-1998; 98AU-0003450.
 FR (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI/) LAVIN M P.
 PA (GAF/) GAFNEY P J.
 PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 DR WPI; 2000-039073/03.
 DR N-PSDB; AAZ29026.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PS Claim 40c; Page 72; 112pp; English.
 CC The present sequence is the proform of the Textillinin protein, Txln 3,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 SO Sequence 83 AA;
 Query Match 81.2%; Score 372; DB 21; Length 83;
 Best Local Similarity 79.5%; Pred. No. 1.3e-37;
 Matches 66; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MSSGGILLLLGLLTMEVLTVPVSSKDHPCFCLPATGSCCKGNVPRFYNNADHQCCKFI 60
 DB 1 MSSGGILLLLGLLTMEVLTVPVSSKDHPCFCLPATGSCCKGNVPRFYNNADHQCCKFI 60
 QY 61 YGGCGGANNFRTIEGKSTCA 83
 DB 61 YGGCGGANNFRTIEGKSTCA 83
 RESULT 3
 ID AAY15141 standard; Protein; 59 AA.
 AC AAY15141;
 DT 07-FEB-2000 (first entry)
 DE Txln 4 plasmin inhibitor protein.
 XX Textillinin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 OS Pseudonaja textilis textilis.
 XX Key Location/Qualifiers
 FM 1..24
 FT /label= leader_peptide
 FT 25..83
 FT /label= Txln-3_protein
 FT /note= "Textillinin-3"
 PN MO9958569-A1.
 PD 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFV/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 DR WPI; 2000-039073/03.
 DR N-PSDB; AAZ29020.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX Claim 8d; Page 69; 112pp; English.
 XX The present sequence is the Textilinin protein, Txln 4, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 XX Sequence 59 AA;
 SQ
 Query Match 74.7%; Score 342; DB 21; Length 59;
 Best Local Similarity 100.0%; Pred. No. 3.9e-34;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 KDHKFCFLPMTSGCKGNVPFYTNADHQCLEKFIYGGCGGNANFTIEGKSTCA 83
 Db 1 KDHKFCFLPMTSGCKGNVPFYTNADHQCLEKFIYGGCGGNANFTIEGKSTCA 59
 RESULT 4
 ID AAY15145 standard; Protein; 83 AA.
 XX AAY15145;
 AC
 XX 07-FEB-2000 (first entry)
 DT
 XX Proform of Txln 1 protein.
 DE
 XX Textilinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KM haematopoietic; cytostatic activity; homology; specificity; control;
 KM Talicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader peptide
 FT 25..83
 FT /label= Txln-1 protein
 FT /note= "Textilinin-1"
 XX
 PN MO9958569-A1.

XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFV/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 DR WPI; 2000-039073/03.
 DR N-PSDB; AAZ29024.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX Claim 40a; Page 71; 112pp; English.
 XX The present sequence is the proform of the Textilinin protein, Txln 1,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
 CC 58% homology with Aprotinin and Talicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 XX Sequence 83 AA;
 SQ
 Query Match 74.5%; Score 341; DB 21; Length 83;
 Best Local Similarity 77.1%; Pred. No. 7.7e-34;
 Matches 64; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MSSGGLLLGLITMEVLTVPSSKDHKFCFLPMTSGCKGNVPFYTNADHQCLEKFI 60
 Db 1 MSSGGLLLGLITMEVLTVPSSKDHKFCFLPMTSGCKGNVPFYTNADHQCLEKFI 60
 QY 61 YGGCGGNANFTIEGKSTCA 83
 Db 61 YGGCGGNANFTIEGKSTCA 83
 RESULT 5
 ID AAY15146 standard; Protein; 83 AA.
 XX AAY15146;
 AC
 XX 07-FEB-2000 (first entry)
 DT
 XX Proform of Txln 2 protein.
 DE
 XX Textilinin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KM haematopoietic; cytostatic activity; homology; specificity; control;
 KM Talicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX Key Location/Qualifiers
 FH
 XX

```

FT Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-2_protein
FT /note= "Textilinin-2"
XX
XX WO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAFN/) GAFNEY P J.
XX
XX Masi PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
XX DR N-PSDB; AA229025.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40b; Page 71; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 2,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln 2 has 43% and
XX 55% homology with Aprotinin and Talcotxin-associated plasmin inhibitor
XX (TAC), respectively. Txln has high specificity for plasmin and low
XX inhibitory efficiency, that can transiently affect the delicate balance
XX between enzymes and inhibitors of the fibrinolytic system, controlling
XX the fluidity of blood. The plasmin inhibitors are useful for alleviating
XX blood loss, following major surgery or trauma. Conjugates of the plasmin
XX inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
XX They have reduced propensity to cause thrombosis.
XX
XX Sequence 83 AA;
XX
XX Query Match 72.7%; Score 333; DB 21; Length 83;
XX Best Local Similarity 74.7%; Pred. No. 7.3e-33;
XX Matches 62; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGLLLGLLTMEVLTVPSSKDPKPCFCELPATGSCGKNVPPFYTNADHHQCLKFI 60
XX Db 1 MSSGGLLLGLLTMEVLTVPSSKDPKPCFCELPATGSCGKNVPPFYTNADHHQCLKFI 60
XX
XX QY 61 YGGCGGNANNFXTKEGKSTCA 83
XX Db 61 YGGCGGNANNFXTKEGKSTCA 83
XX
XX RESULT 6
XX ID AAY15149 standard; Protein; 83 AA.
XX
XX AAY15149;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 5 protein.
XX
XX Textilinin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX

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```

XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..24
XX FT /label= Leader_peptide
XX FT Protein 25..83
XX FT /label= Txln-5_protein
XX FT /note= "Textilinin-5"
XX
XX WO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASI P P.
XX (LAVI/) LAVIN M F.
XX (GAFN/) GAFNEY P J.
XX
XX Masi PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
XX DR N-PSDB; AA229028.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40e; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 5,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 83 AA;
XX
XX Query Match 69.2%; Score 317; DB 21; Length 83;
XX Best Local Similarity 72.3%; Pred. No. 6.6e-31;
XX Matches 60; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGLLLGLLTMEVLTVPSSKDPKPCFCELPATGSCGKNVPPFYTNADHHQCLKFI 60
XX Db 1 MSSGGLLLGLLTMEVLTVPSSKDPKPCFCELPATGSCGKNVPPFYTNADHHQCLKFI 60
XX
XX QY 61 YGGCGGNANNFXTKEGKSTCA 83
XX Db 61 YGGCGGNANNFXTKEGKSTCA 83
XX
XX RESULT 7
XX ID AAY15150 standard; Protein; 83 AA.
XX
XX AAY15150;
XX
XX 07-FEB-2000 (first entry)
XX
XX Proform of Txln 6 protein.
XX

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XX XX Textilin protein; Txln 6; plasmin inhibitor; single stage inhibitor;
XX KW Australian brown snake; conserved cysteine residue; stability; control;
XX KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX KW fluidity of blood; alleivate; blood loss; major surgery; trauma; enzyme;
XX KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX KM reduced propensity; thrombosis.
XX OS
XX Pseudonaja textilis textilis.
XX FH Key
XX FH Location/Qualifiers
XX FT 1..24
XX FT /label= Leader peptide
XX FT 25..83
XX FT /label= Txln-6 protein
XX FT /note= "Textilin-6"
XX PN
XX PN MO958569-A1.
XX PD 18-NOV-1999.
XX PP 07-MAY-1999; 99MO-AU00343.
XX PR 11-MAY-1998; 98AU-0003450.
XX XX
XX XX (UYOU ) UNIV QUEENSLAND.
XX PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX PA (MASC/) MASC P P.
XX PA (LAVI/) LAVIN M F.
XX PA (GAFF/) GAFFNEY P J.
XX PI Maeci PP, Lavin MF, Gaffney PJ, Sorokina NI, Philippovich IV,
XX XX WPI; 2000-039073/03.
XX DR N-PSDB; AAZ29029.
XX PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX PT agents -
XX PS
XX PS Claim 40f; Page 72; 112pp; English.
XX CC The present sequence is the proform of the Textilin protein, Txln 6,
XX CC that is a single stage competitive inhibitor of plasmin. It is isolated
XX CC from the Australian brown snake, Pseudonaja textilis textilis. It has
XX CC six conserved cysteine residues, that endow them great stability. This
XX CC sequence has haematopoietic and cytostatic activity. Txln has high
XX CC specificity for plasmin and low inhibitory efficiency, that can
XX CC transiently affect the delicate balance between enzymes and inhibitors
XX CC of the fibrinolytic system, controlling the fluidity of blood. The
XX CC plasmin inhibitors are useful for alleviating blood loss, following
XX CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX CC propensity to cause thrombosis.
XX SQ
XX SQ Sequence 83 AA;
XX
XX Query Match 67.2%; Score 308; DB 21; Length 83;
XX Best Local Similarity 69.9%; Pred. No. 8.2e-30;
XX Matches 58; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
XX
XX 1 MSSGGILLILGLTLMEVLTTPVSSKHDKPCFLPABTSSCKGNVRFYNNADHQCILKEI 60
XX 1 MSSGGILLILGLTLMEVLTTPVSSKHDKPCFLPADIGPWMDFTGAFHYSPREHECIEFI 60
XX
XX 61 YGGCGGNANPKRTIEKSGTCA 83
XX 61 YGGCGGNANPKRTIEKSGTCA 83
XX
XX RESULT 8
XX ID AA15140 standard; Protein; 59 AA.
XX

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AC	AA15140;
XX	
DT	07-FEB-2000 (first entry)
XX	
DE	Txln 3 Plasmin inhibitor protein.
XX	
KW	Textilinin protein; Txln 3, plasmin inhibitor; single stage inhibitor;
KW	Australian brown snake; conserved cysteine residue; stability; control;
KW	haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
KW	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KW	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX	reduced propensity; thrombosis.
OS	Pseudonaja textilis textilis.
XX	
PN	WO958569-A1.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-AU00343.
XX	
PR	11-MAY-1998; 98AU-0003450.
XX	
PA	(UYOU) UNIV QUEENSLAND.
PA	(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA	(MASC/) MASC P P.
PA	(LAVI/) LAVIN M P.
PA	(GAF/) GAFFNEY P J.
XX	
PI	Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
DR	WPI, 2000-039073/03.
DR	N-PSDB; AA229019.
PT	Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT	agents -
XX	
PS	Claim 8c, Page 69, 112PP; English.
XX	
CC	The present sequence is the Textilinin protein, Txln 3, that is a
CC	single stage competitive inhibitor of plasmin. It is isolated from the
CC	Australian brown snake, Pseudonaja textilis textilis. It has six
CC	conserved cysteine residues, that endow them great stability. This
CC	sequence has haematopoietic and cytosolic activity. Txln has high
CC	specificity for plasmin and low inhibitory efficiency, that can
CC	transiently affect the delicate balance between enzymes and inhibitors
CC	of the fibrinolytic system, controlling the fluidity of blood. The
CC	plasmin inhibitors are useful for alleviating blood loss, following
CC	major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC	anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC	propensity to cause thrombosis.
XX	
SQ	Sequence 59 AA:
Query Match	55.9%; Score 256; DB 21; Length 59;
Best Local Similarity	71.2%; Pred. No. 1.2e-23;
Matches 42; Conservative	7; Mismatches 10; Indels 0; Gaps 0;
DB	
25	KDHKFEELPAETGSSCKGNVPRFYNDHHOCLKFTYGGCGGANNRFTIEGGSTCA 83
1	KDRNPFCKLPATRCNCAKIPRFYNNRHOCLIEFLYGGCGGANNRFTIKCESTCA 59
RESULT 9	
AA15151	
ID	AA15151 standard; Protein; 60 AA.
XX	
XX	AA15151;
XX	
DT	07-FEB-2000 (first entry)
DE	Plasmin inhibitor Txln 1, partial protein sequence.
XX	


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XX XX Pseudonaja textilis textilis.
OS
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= leader_peptide
PT 25..60
FT /label= Partial-Txln-1-protein
PT /note= "Plasmin inhibitor"
TX WO958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIT QUEENSLAND.
PA (NABIC-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC-) MSCI P P.
PA (LAVI/) LAVIN M F.
PA (GAFNE/) GAFNEY P J.
PI Maeci PP, Lavin MF, Gafney PJ, Sorokina NI, Filipovich IV;
XX DR WP1; 2000-039073/03.
XX DR N-PSDB; AAZ29030.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents -
XX
XX Example 2; Page 108; 112pp; English.
XX
XX The present sequence is the partial Txln 1, Textilinin protein sequence.
CC It is obtained by sequence analysis of the 5' and 3'RACE products. It is
CC a single stage competitive inhibitor of plasmin. It is isolated from the
CC Australian brown snake, Pseudonaja textilis textilis. It has six
CC conserved cysteine residues, that endow them great stability. This
CC sequence has haematopoietic and cytostatic activity. Txln 1 has 45' and
CC 58' homology with Apoptin and Telocorin-associated plasmin inhibitor
CC (TAC), respectively. Txln has high specificity for plasmin and low
CC inhibitory efficiency. Txln can transiently affect the delicate balance
CC between enzymes and inhibitors of the fibrinolytic system, controlling
CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
CC blood loss, following major surgery or trauma. Conjugates of the plasmin
CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
CC They have reduced propensity to cause thrombosis.
XX
XX Sequence 60 AA:
SQ
XX
XX Query Match 52.2%; Score 239; DB 21; Length 60;
XX Best Local Similarity 73.3%; Pred. No. 1.5e-21;
XX Matches 44; Conservative 5; Mismatches 11; Indels 0; Gaps 0
OY 1 MSSGGILLILGLTLMEVLTPVSSKDHPKCELPARETSCKGNVPAPFYNNADHOCLEFI 60
DB 1 MSSGGILLILGLTLMEVLTPVSSKDHPKCELPARETSCKGNVPAPFYNNADHOCLEFI 60
AAAY15138
ID AAAY15138 standard; Protein; 59 AA.
AC AAAY15138;
XX
DT 07-FEB-2000 (first entry)

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```

XX XX      Txln 1 Plasmin inhibitor protein.
DE XX
XX XX      Textillinin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
XX XX      Australian brown snake; conserved cysteine residue; stability; control;
XX XX      haematopoietic; cytostatic activity; homology; specificity; Aprotinin;
XX XX      Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
XX XX      fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX XX      fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX XX      reduced propensity; thrombosis.
OS XX
XX XX      Pseudonaja textilis textilis.
XX XX      WO95958569-A1.
XX XX      18-NOV-1999.
PD XX
XX XX      07-MAY-1999; 99WO-AU00343.
XX XX      11-MAY-1998; 98AU-0003450.
PR XX
XX XX      (UYOU ) UNIV QUEENSLAND.
XX XX      (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX XX      (MASC/) MASC P P.
XX XX      (LAVI/) LAVIN M F.
XX XX      (GAFF/) GAFFNEY P J.
PI XX
XX XX      Maaci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
DR XX      WPI; 2000-039073/03.
DR XX      N-PSDB; AAZ29017.
XX XX
XX XX      Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT XX      agents -
PS XX
XX XX      Claim 8a; Page 68; 112pp; English.
XX XX
XX XX      The present sequence is the Textillinin protein, Txln 1, that is a
CC XX      single stage competitive inhibitor of plasmin. It is isolated from the
CC XX      Australian brown snake, Pseudonaja textilis textilis. It has six
CC XX      conserved cysteine residues, that endow them great stability. This
CC XX      sequence has haematopoietic and cytostatic activity. Txln 1 has 458 and
CC XX      588 homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
CC XX      (TAC), respectively. Txln has high specificity for plasmin and low
CC XX      inhibitory efficiency, that can transiently affect the delicate balance
CC XX      between enzymes and inhibitors of the fibrinolytic system, controlling
CC XX      the fluidity of blood. The plasmin inhibitors are useful for alleviating
CC XX      blood loss, following major surgery or trauma. Conjugates of the plasmin
CC XX      inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
CC XX      They have reduced propensity to cause thrombosis.
CC XX
SQ XX      Sequence 59 AA;
XX XX
XX XX      Query Match 49.1%; Score 225; DB 21; Length 59;
XX XX      Best Local Similarity 67.8%; Pred. No. 7.4e-20;
XX XX      Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
OY XX
XX XX      25 KDRKFCFELPAETGSCKGNVRFYYNADHQCLEFYIGGCGGANNFTEEGKSTCA 83
XX XX      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX XX      1 KDRDFGCLPADTGPCRVRFPSFYFNPDEKKCLFHYIGGCGGANNFITKECESTCA 59
XX XX
XX XX      RESULT 11
XX XX      ID AA15153
XX XX      AA15153 standard; Protein; 60 AA.
XX XX
XX XX      AA15153;
XX XX
XX XX      07-FEB-2000 (first entry)
XX XX
XX XX      Plasmin Inhibitor Txln 1, encoded by partial cDNA sequence.
XX XX
XX XX      Textillinin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
XX XX

```

Key	Location/Qualifiers
Misc-difference 24	/note= "encoded by TTG"
Misc-difference 47	/note= "encoded by GAT"
Misc-difference 49	/note= "encoded by ATG"
WO958569-A1.	
18-NOV-1999.	
07-MAY-1999;	99WO-AU00343.
11-MAY-1998;	98AU-0003450.
(UYOU) UNIV QUEENSLAND.	
(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.	
(MASC/) MASC P P.	
(LAVI/) LAVIN M F.	
(GAF/) GAFNEY P J.	
Masci P P, Lavin M F, Gafney P J, Sorokina N I, Filipovich I V;	
WP1: 2000-039073/03.	
N-PSDB: MAZ23047.	
Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor agents -	
Disclosure; Fig 6; 112pp; English.	
The present amino acid sequence is the Tx1n 1, Textillin protein	
inhibitor of the partial cDNA sequence. It is a single stage competitive	
inhibitor of plasmin. It is isolated from the Australian brown snake,	
Pseudonaja textilis textilis. Tx1n has high specificity for plasmin and	
low inhibitory efficiency that can transiently affect the delicate	
balance between enzymes and inhibitors of the fibrinolytic system,	
controlling the fluidity of blood. The plasmin inhibitors are useful for	
alleviating blood loss, following major surgery or trauma. Conjugates of	
the plasmin inhibitor and an anti-fibrin antibody are useful as	
anti-tumour agents. They have reduced propensity to cause thrombosis.	
Sequence 60 AA;	
Query Match 47.6%; Score 218; DB 21; Length 60;	
Best Local Similarity 64.4%; Pred. No. 5.4e-19;	
Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;	
25 KDHPFCGLPVTGSCGKGNVPRFYNNAAHOCLEKTYIGCGGNANPFTIEGKSTCA 83	
2 KDRPFCGLPDTGFCVRVPRFSPYINPDKCLPFTYIGCGGNANPFTIEGKSTCGS 60	
RESULT 12	
ID AAY15139 standard; Protein; 59 AA.	
AAY15139;	
07-FEB-2000 (first entry)	
Tx1n 2 Plasmin inhibitor protein.	
Textillin protein; Tx1n 2; plasmin inhibitor; single stage inhibitor;	

[illegible]

```

OS Synthetic.
PN WO9620278-A2.
PD 04-JUL-1996.
XX
XX
PP 15-DEC-1995; 95WO-US16349.
XX
XX 16-DEC-1994; 94US-0356160.
XX
XX (PROT-) PROTEIN ENG CORP.
PA
XX
PI Guerman SK, Kent RB, Ladner RC, Ley AC, Markland W;
PI Roberts BL;
PI
XX
DR WP1; 1996-321851/32.
XX
PT New engineered inhibitors of human neutrophil elastase - contg.
PT aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or
PT other respiratory disorders
XX
XX
PS Example 23; Page 47; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the
CC elimination of pathogens and the restructuring of connective tissue.
CC In cases of reduction of the circulating alpha-1-protease inhibitor
CC (API or alpha antitrypsin), or the inactivation of API by oxidation
CC (smokers emphysema), extensive destruction of the lung tissue may
CC result from uncontrolled elastolytic activity of human neutrophil
CC elastase. Other respiratory disorders such as cystic fibrosis are
CC thought to be caused by human neutrophil elastase release by
CC neutrophils. The genetically engineered human derived Kunitz
CC domains can be used to treat such respiratory disorders. See
CC AAR99146-R99211.
XX
XX Sequence 58 AA;
SQ
Query Match 46.1%; Score 211; DB 17; Length 58;
Best Local Similarity 68.5%; Pred. No. 3, 7e-18;
Matches 37; Conservative 4; Mismatches 13; Indels 0; Gaps 0
OY 28 PKECELPAETGSCCKGVPRFTYNADHQCCKRTIYGGCGGNANFTIEBQSTC 81
Db 2 PDFCLLPATGTGCRAMIPRFYFNAXSGKCEPIYGGCGGNANFTIEBQSTC 55
RESULT 14
AY15142
AY15142 standard; Protein; 59 AA.
AY15142;
AY15142;
DT 07-FEB-2000 (first entry)
XX
XX Txln 5 Plasmin inhibitor protein.
DE
XX
XX Textilinin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
KM Australian brown snake; conserved cysteine residue; stability; control;
KM haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
OS
XX WO9958569-A1.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-AU00343.
PP
XX
XX 11-MAY-1998; 98AU-0003450.
PR

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(UNIV QUEENSLAND.
NAB(-) NAT INST BIOLOGICAL STANDARDS & CO.
(MASC/) MASC P P.
(LAVI/) LAVIN M F.
(GAF/) GAFNEY P J.

Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
WPI; 2000-039073/03.
DR N-PSDB; AA229021.

Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
agents -
Claim 8e; Page 69; 112pp; English.

The present sequence is the Textillin protein, Txln 5, that is a
single stage competitive inhibitor of plasmin. It is isolated from the
Australian brown snake, Pseudonaja textilis textilis. It has six
conserved cysteine residues, that endow them great stability. This
sequence has haematopeletic and cytostatic activity. Txln has high
specificity for plasmin and low inhibitory efficiency, that can
transiently affect the delicate balance between enzymes and inhibitors
of the fibrinolytic system, controlling the fluidity of blood. The
plasmin inhibitors are useful for alleviating blood loss, following
major surgery or trauma. Conjugates of the plasmin inhibitor and an
anti-fibrin antibody are useful as anti-tumour agents. They have reduced
propensity to cause thrombosis.

Sequence 59 AA;

Query Match 43.9%; Score 201; DB 21; Length 59;
Best Local Similarity 61.0%; Pred. No. 6.3e-17;
Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

25 KDHHKPEELPARGSCSKCNVPRFYNNADHHCCKEYIGGGGANNFETIEEGSTCA 83
Db 1 KDRPKFELLPTGTSCSDFTGAFHYSTRDRCLEIFITGGCGGNANFTIECESTCA 59

RESULT 15
AA15154
ID AA15154 standard; Protein; 60 AA.
XX AC AAY15154;
XX XX
DT 07-FEB-2000 (first entry)

Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.

Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
Australian brown snake; conserved cysteine residue; stability; control;
haematopoietic; cytostatic activity; homology; enzyme;
fluidity of blood; alleviate; blood loss; major surgery; trauma;
fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
inhibitory efficiency; reduced propensity; thrombosis.

Pseudonaja textilis textilis.

Key Location/Qualifiers
Misc-difference 24 /note= "encoded by TTG"
Misc-difference 45 /note= "encoded by GAT"
Misc-difference 49 /note= "encoded by ATG"
Misc-difference 59 /note= "encoded by CCN"

MO3958569-A1.
18-NOV-1999.

```

XX 07-MAY-1999; 99WO-AU00343.
PF
XX
PR 11-MAY-1998; 98AU-0003450.
XX
PA (UYOU ) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC/) MASC P P.
PA (LAVI/) LAVIN M F.
PA (GAFNEV) GAFNEV P J.
PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX DR N-PSDB; AAZ29048.
XX
PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
agents -
XX
PS Disclosure; Fig 7; 112pp; English.
XX
CC The present amino acid sequence is the Txln 2, Textilinin protein
CC encoded by the partial cDNA sequence. It is a single stage competitive
CC inhibitor of plasmin. It is isolated from the Australian brown snake,
CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
CC low inhibitory efficiency that can transiently affect the delicate
CC balance between enzymes and inhibitors of the fibrinolytic system,
CC controlling the fluidity of blood. The plasmin inhibitors are useful for
CC alleviating blood loss, following major surgery or trauma. Conjugates of
CC the plasmin inhibitor and an anti-fibrin antibody are useful as
CC anti-tumour agents. They have reduced propensity to cause thrombosis.
XX
SQ Sequence 60 AA:
Query Match 42.1%; Score 193; DB 21; Length 60;
Best Local Similarity 59.6%; Pred. No. 6.1e-16;
Matches 34; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
QY 25 KDHPKPCELPAETGSCCKGNVPRFYNNADHOCLEKPIYGGCGGNANNFKTIERGKSTC 81
DB 2 KDRPELCPLPDPTGFCRVRFPSPFTYNPDQKLEFIYGGCEENANAFITKBECESTC 58

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Search completed: January 23, 2004, 10:24:36
 Job time : 40.0387 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 7.59859 Seconds
(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179a-16

Perfect score: 457
Sequence: 1 MSQGGILLGLTLMEVLT.....CEGNANFTRKECESTCAA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt 41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	49.8	85	1	IVB2_BUNMU
2	214	46.8	65	1	IVB3_VITPA
3	204	44.6	62	1	IP52_ANESU
4	201	44.0	57	1	IVB2_NAJNI
5	201	44.0	61	1	IVB1_VITPA
6	198	43.3	57	1	IVB2_HEMAA
7	195	42.7	62	1	IVBT_HERMA
8	195	42.7	85	1	IVBT_BUNMU
9	194	42.5	57	1	IVBT_NAJNI
10	192	42.0	65	1	IVB1_BUNPA
11	189	41.4	110	1	IBP_GARCR
12	188.5	41.2	230	1	TPP2_MOUSE
13	188	41.1	58	1	ISIK_HELPO
14	187.5	41.0	55	1	SPTI_BOMMO
15	180	39.4	252	1	SPTI_HUMAN
16	179	39.2	58	1	AXPI_ANTAF
17	179	39.2	59	1	IVBE_DENPO
18	178	38.9	60	1	IVB2_DABRU
19	172	37.6	302	1	TPPI_RAT
20	171	37.4	300	1	TPPI_RABIT
21	171	37.4	306	1	TPPI_MOUSE
22	170.5	37.3	122	1	UPPI_PIG
23	170	37.2	235	1	TPP2_HUMAN
24	169	37.0	57	1	IVBK_DENAN
25	169	37.0	304	1	TPPI_MACMU
26	168	36.8	57	1	IVBC_DENPO
27	168	36.8	58	1	IVBC_OPHHA
28	168	36.8	133	1	BPTI_HUMAN
29	167	36.5	58	1	AXP2_ANTAF
30	166.5	36.4	100	1	BPTI_BOVIN
31	166	36.3	513	1	SPTI_HUMAN
32	165	36.1	57	1	SPTI_SARBU
33	163.5	35.8	100	1	BPT2_BOVIN

34	163	35.7	252	1	SPT2_MOUSE	O9MU03 mus musculus
35	162.5	35.6	69	1	CRPT_BOOMI	P81162 boophilus m
36	162	35.4	304	1	TPPI_HUMAN	P10646 homo sapien
37	160	35.0	3176	1	CA36_HUMAN	P12111 homo sapien
38	153	33.5	57	1	IVBE_DENPO	P00983 dendroaspis
39	152	33.3	60	1	IBPS_BOVIN	P00975 bos taurus
40	152	33.3	770	1	A4_MOUSE	P12023 m amyloid b
41	151	33.0	507	1	SPT1_MOUSE	O9T097 mus musculus
42	150.5	32.9	352	1	AMBP_HUMAN	P02760 homo sapien
43	150	32.8	76	1	A4_MACMU	P29216 macaca mula
44	150	32.8	751	1	A4_SAISC	O95241 s amyloid b
45	150	32.8	770	1	A4_HUMAN	P05067 h amyloid b

ALIGNMENTS

RESULT 1

IVB2_BUNMU	STANDARD; Q9PRV8; Q9PTA3;	PRT;	85 AA.
AC P00989; Q42299; Q9PRV8; Q9PTA3;			
DT 21-JUL-1986 (Ref. 01, Created)			
DT 15-JUN-1998 (Ref. 36, Last sequence update)			
DT 15-SEP-2003 (Ref. 42, Last annotation update)			
DE Beta bungarotoxin B2 chain precursor.			
OS Bungarus multicinctus (Many-banded krait).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC Elapidae; Bungarinae; Bungarus.			
CC NCBI_TaxID=8616;			
CX (1)			
RN SEQUENCE FROM N.A.			
RC TISSUE=Venom gland;			
RP MEDLINE=20363696; PubMed=10903499;			
RX Wu P.-F., Chang L.-S.;			
RA "Genetic structures of A chain and B chain of beta-bungarotoxin from			
RT Taiwan banded krait (Bungarus multicinctus). A chain genes and B chain			
RT genes do not share a common origin.";			
RL Eur. J. Biochem. 267:4668-4675 (2000).			
RN (3)			
RP SEQUENCE OF 25-85.			
RC TISSUE=Venom;			
RX MEDLINE=82239269; PubMed=7096304;			
RA Kondo K., Toda H., Narita K., Lee C.-Y.;			
RT "Amino acid sequence of beta 2-bungarotoxin from Bungarus			
RL J. Biochem. 91:1519-1530 (1982).			
RN (4)			
RP SEQUENCE OF 25-63.			
RX MEDLINE=95031955; PubMed=7945237;			
RA Chu C.-C., Chu S.-T., Chen S.-W., Chen Y.-H.;			
RT "The non-phospholipase A2 subunit of beta-bungarotoxin plays an			
RT important role in the phospholipase A2-independent neurotoxic effect:			
RT characterization of three isoforms with a common phospholipase A2			
RT subunit.";			
RL Biochem. J. 303:171-176 (1994).			
RN (5)			
RP REVIEW.			
RX MEDLINE=20396379; PubMed=10936627;			
RA Rowan B.G.;			
RT "What does beta-bungarotoxin do at the neuromuscular junction?";			
RL Toxicon 39:107-118 (2001).			
CC -1- FUNCTION: Beta-2 bungarotoxin is a presynaptic neurotoxin of the			
CC venom. The B chain is homologous to venom basic protease			
CC inhibitors but has no protease inhibitor activity and is non-			

CC toxic.
 CC -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
 CC The A chains have phospholipase A2 activity and the B chains show
 CC homology with the basic protease inhibitors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y12101; CAB62810.1; -.
 CC EMBL; AJ251224; CAB62504.1; -.
 CC PDB; 1BUN; 03-APR-96.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF00014; Kunitz_BPTI_1.
 CC ProDom; PD000222; Kunitz_BPTI_1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 CC Toxin; Neurotoxin; Presynaptic neurotoxin; Signal; 3D-structure.
 CC SIGNAL.
 CC FT CHAIN 1 24
 CC FT DOMAIN 25 85 BETA BUNGAROTOXIN B2 CHAIN.
 CC FT DISULFID 31 81 BPTI/KUNITZ INHIBITOR.
 CC FT DISULFID 31 81 BY SIMILARITY.
 CC FT DISULFID 40 64 BY SIMILARITY.
 CC FT DISULFID 56 77 BY SIMILARITY.
 CC FT DISULFID 79 79 INTERCHAIN (WITH AN A CHAIN) (BY
 CC FT ACT SITE 41 42 REACTIVE BOND (BY SIMILARITY).
 CC FT CONFLICT 44 44 MISSING (IN REF. 3).
 CC FT CONFLICT 65 70 NNGNHN -> DGDHGN (IN REF. 3).
 CC FT CONFLICT 82 83 LE -> EL (IN REF. 3).
 CC FT SEQUENCE 85 AA; 9568 MW; FE95A59AF92B22AA CRC64;
 SQ
 Query Match 49.9%; Score 228; DB 1; Length 85;
 Best Local Similarity 54.3%; Pred. No. 2.2e-19;
 Matches 44; Conservative 9; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MSSGGLLLLTGTLTMBVLTTPVSSKDRPFCELPADTGCRCRFRPFYNNPDEKCLERTI 60
 DB 1 MSSGGLLLLTGTLTCAELTPVSSRRKHPDCRPPDTKICQTVRAFYKPSAKGVQPR 60
 QY 61 YGCGEGNANNFITKEECSTC 81
 DB 61 YGCGNGNGNHFKSDHLCREC 81
 RESULT 2
 IVB3_VIPAA STANDARD; PRT; 65. AA.
 AC P00952;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).
 OS Vipera ammodytes ammodytes (Western sand viper).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Viperinae; Vipera.
 OC NCBI_TaxId=8705;
 OC [1]
 RP SEQUENCE.
 RC Tissue=Venom;
 RA Rittenja A., Meloun B., Gubensek F.;
 RT "The primary structure of Vipera ammodytes venom chymotrypsin
 RT inhibitor.";
 RL Biochim. Biophys. Acta 746:138-145(1983).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC PIR; A01223; TIVYIC.
 CC DR HSSP; P31713; ISHP.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF00014; Kunitz_BPTI_1.
 CC ProDom; PD000222; Kunitz_BPTI_1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 CC Serine protease inhibitor.
 CC FT DISULFID 7 57
 CC FT DISULFID 16 40
 CC FT DISULFID 32 53
 CC FT ACT SITE 17 18
 CC SEQUENCE 65 AA; 7556 MW; 9D526F83B7CC57 CRC64;
 SQ
 Query Match 46.8%; Score 214; DB 1; Length 65;
 Best Local Similarity 62.7%; Pred. No. 6.6e-18;
 Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
 QY 25 KDRPFCFLPADTGCRCRFRPFYNNPDEKCLERTIYGCGEGNANNFITKEECSTCA 83
 DB 1 RDRPFCFLPADTGCRCRFRPFYNNPDEKCLERTIYGCGEGNANNFITKEECSTCA 59
 RESULT 3
 IP52_ANESU STANDARD; PRT; 62. AA.
 AC P10280;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Protease inhibitor 5 II (SAs II).
 OS Anemona sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinaria;
 OC Nymphaea; Actiniidae; Anemona.
 CC NCBI_TaxId=6108;
 RN [1]
 RP SEQUENCE OF 1-59.
 RA Wunderer G., Machleidt W., Fritze H.;
 RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
 RT Anemona sulcata.";
 RL Meth. Enzymol. 80:816-820(1981).
 RN [2]
 RP SEQUENCE.
 RA Krebs H.C., Habermehl G.G.;
 RT "Isolation and structural determination of a hemolytic active peptide
 RT from the sea anemone Metridium senile.";
 RL Naturwissenschaften 74:1395-1396(1987).
 CC -1- FUNCTION: INHIBITOR OF KALLIKREIN.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC PIR; S07451; S07451.
 CC DR HSSP; P31713; ISHP.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF00014; Kunitz_BPTI_1.
 CC ProDom; PD000222; Kunitz_BPTI_1.
 CC PRINTS; PR00759; BASICPTASE.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 CC Serine protease inhibitor.
 CC FT DISULFID 5 55
 CC FT DISULFID 14 38
 CC FT DISULFID 30 51
 CC FT ACT SITE 13 16
 CC FT VARIANT 13 13
 CC FT VARIANT 16 16
 CC FT VARIANT 17 17
 CC FT VARIANT 17 17
 CC FT VARIANT 25 25
 CC FT VARIANT 28 28
 CC FT VARIANT 39 39
 CC SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match	44.6%	Score 204	DB 1	Length 62
Best Local Similarity	66.7%	Pred. No. 8.8e-17		
Matches 34	Conservative 3	Mismatches 14	Indels 0	Gaps 0
Qy	31	CELPADTGPCVRPPSPFYNNDEKKCLBPIYGGCGGNANNPITYKECESTC	81	
Db	5	CELPKRVGPGCRAPFRPRYYNNSSSKRCERFIYGGCGGNANNPITYKECEKVC	55	
RESULT 4				
IBV2_NAJNI	STANDARD	PRT	57 AA	
AC	P00986			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Venom basic protease inhibitor II.			
OS	Naja nivea (Cape cobra).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Elapidae; Elapinae; Naja.			
OC	NCBI_TaxID=8655;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=76237547; PubMed=950337;			
RA	Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;			
RT	"Snake venom proteinase inhibitors. III. Isolation of five			
RT	polypeptide proteinase inhibitors from the venoms of Hemachatus haemachatus			
RT	(Ringhals cobra) and Naja nivea (Cape cobra) and the complete amino			
RT	acid sequences of two of them."			
J.	Biochem. 79:559-578(1976).			
-1-	FUNCTION: The activity of this inhibitor is probably similar to			
-1-	that of bovine basic protease inhibitor.			
-1-	SUBCELLULAR LOCATION: Secreted.			
-1-	SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
CC	CC			
DR	HSSP; P00981; IDTK.			
DR	PIR; A01217; TINDVC.			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI_1.			
DR	ProDom; PD000222; Kunitz_BPTI_1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
KW	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
FT	Serine protease inhibitor.			
FT	DISULFID 5 55	BY SIMILARITY.		
FT	DISULFID 14 38	BY SIMILARITY.		
FT	DISULFID 30 51	BY SIMILARITY.		
FT	ACT SITE 15 16	REACTIVE BOND (BY SIMILARITY).		
SO	SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;			
Query Match	44.0%	Score 201	DB 1	Length 57
Best Local Similarity	63.6%	Pred. No. 1.8e-16		
Matches 35	Conservative 6	Mismatches 14	Indels 0	Gaps 0
Qy	27	RPDFCELADGPGCRVRPPSPFYNNDEKKCLBPIYGGCGGNANNPITYKECESTC	81	
Db	1	RPRFCELPAETGLCARIRSFYNNRAAQQCLFIYGGCGGNANNPITYKECHTC	55	
RESULT 5				
IBV1_VIPAA	STANDARD	PRT	61 AA	
AC	P00991			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Venom basic protease inhibitor I (Venom trypsin inhibitor I).			
OS	Vipera ammodytes ammodytes (Western sand viper).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Viperidae; Viperinae; Vipera.			

OX	NCBI_TaxID=8705;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Venom;
RC	MEDLINE=84053385; PubMed=6639951;
RA	Ritona A., Meloun B., Gubensek P.;
RT	"The primary structure of Vipera ammodytes venom trypsin inhibitor I";
RL	Biochim. Biophys. Acta 748:429-435(1983).
CC	-1- FUNCTION: This protein inhibits trypsin and kallikrein.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR	PIR; A01222; TIVIT1.
DR	HSSP; P31713; tSHP.
DR	InterPro; IPR002223; Kunitz_BPTI.
DR	Pfam; PF00014; Kunitz_BPTI_1.
DR	ProDom; PD000222; Kunitz_BPTI_1.
DR	SMART; SMO0131; KU; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
KW	Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT	MOD_RSS 1 1
FT	DISULFID 7 57
FT	DISULFID 16 40
FT	DISULFID 32 53
SO	SEQUENCE 61 AA; 6865 MW; PC0285P57PE3795 CRC64;
Query Match	44.0%; Score 201; DB 1; Length 61;
Best Local Similarity	57.6%; Pred. No. 1.9e-16;
Matches 34; Conservative	5; Mismatches: 20; Indels 0; Gaps 0;
OY	25 KDQDREGLPADTGPCVRRPPSYNDDEKCEFIYGCGEGNNPFTRKECSTCA 83
DB	1 QDHKKCYLPADPCCKAHIPRFYDSASNKCNKFITGGCPGANNFKTMDECRQTGA 59
RESULT 6	
ID	IBV2_HEMHA STANDARD; PRT; 57 AA.
AC	P00985;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Venom basic protease inhibitor II. (Sepedon haemachatus).
OS	Haemachatus haemachatus (Ringhals) (Sepedon haemachatus).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Leptocephala; Squamata; Sclerozoosae; Serpentes; Colubroidea;
OC	Elapidae; Elapinae; Hemachatus.
OX	NCBI_TaxID=8626;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=76237547; PubMed=950337;
RA	Hokama Y., Iwanaga S., Tatsuki T., Suzuki T.;
RT	"Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitors from the venoms of Hemachatus haemachatus (Ringhal's cobra) and Naja nivea (Cape cobra) and the complete amino acid sequences of two of them.";
RL	J. Biochem. 79:559-578(1976).
CC	-1- FUNCTION: The activity of this inhibitor is similar to that of bovine basic protease inhibitor.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR	PIR; A01216; TIRIV2.
DR	HSSP; P00981; IDTK.
DR	InterPro; IPR002223; Kunitz_BPTI.
DR	Pfam; PF00014; Kunitz_BPTI_1.
DR	ProDom; PD000222; Kunitz_BPTI_1.
DR	SMART; SMO0131; KU; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
KW	Serine protease inhibitor.
FT	DISULFID 5 55
FT	DISULFID 14 38
FT	BY SIMILARITY. BY SIMILARITY.

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FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7F2A CRC64;

Query Match
Best Local Similarity 43.3%; Score 198; DB 1; Length 57;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 27 RPDCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTC 81
Db 1 RPDCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTC 55

RESULT 7
ID IVBT_ERIMA STANDARD; PRT; 62 AA.
AC P24541;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom trypsin inhibitor.
OS Eristocophis macmahoni (Leaf-nosed viper).
OC Bufoyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Eristocophis.
OX NCBI_Taxid=8702;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=92077130; PubMed=1743283;
RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
RT "Purification and characterization of a Kunitz-type trypsin inhibitor
from leaf-nosed viper venom."
RL FEBS Lett. 294:141-143(1991).
CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR: S19327; S19327.
DR HSSP: P00981; IDTK.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICTPASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 2 52 BY SIMILARITY.
FT DISULFID 11 35 BY SIMILARITY.
FT DISULFID 27 48 BY SIMILARITY.
FT ACT SITE 12 13 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 62 AA; 6772 MW; 0A2BD0ADB20DF938 CRC64;

Query Match
Best Local Similarity 42.7%; Score 195; DB 1; Length 62;
Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 30 RCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTCA 83
Db 1 RCELPADTGPCRVPRPSFYNDPEKKCLFITYGGEGNANNITKEEGESTCA 54

RESULT 8
ID IVBT_BUNMU STANDARD; PRT; 85 AA.
AC P00987; O42298; P00988;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta bungarotoxin B1 chain, major component precursor.
OS Bungarus multicinctus (Many-banded krait).
OC Bufoyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;

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OC Elapidae; Bungarinae; Bungarus.
OX NCBI_Taxid=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=98359733; PubMed=9693106;
RA Wu P.-F., Wu S.N., Chang C.-C., Chang L.-S.;
RT "Cloning and functional expression of B chains of beta-bungarotoxins
from Bungarus multicinctus (Taiwan banded krait).";
RL Biochem. J. 334:87-92(1998).
RN [2]
RP SEQUENCE OF 25-85.
RC TISSUE=Venom;
RX MEDLINE=78109400; PubMed=624701;
RA Kondo K., Narita K., Lee C.-Y.;
RT "Amino acid sequences of the two polypeptide chains in beta1-
bungarotoxin from the venom of Bungarus multicinctus.";
RL J. Biochem. 83:101-115(1978).
RN [3]
RP MUTAGENESIS OF CYS-32.
RX MEDLINE=21589307; PubMed=11732693;
RA Wu P.-F., Chang L.-S.;
RT "Expression of A chain and B chain of beta-bungarotoxin from taiwan
banded krait: the functional implication of the interchain disulfide
bond between A chain and B chain.";
RL J. Protein Chem. 20:413-421(2001).
RN [4]
RP REVIEW.
RX MEDLINE=20396379; PubMed=10936627;
RA Rowan B.G.;
RT "What does beta-bungarotoxin do at the neuromuscular junction?";
RL Toxicol 39:107-118(2001).
CC -1- FUNCTION: Beta-1 bungarotoxin is a presynaptic neurotoxin of the
venom. The B chain is homologous to venom basic protease
inhibitors, but has no protease inhibitor activity and is non-
toxic.
CC -1- SUBUNIT: Dimer of dissimilar chains linked by a disulfide bond.
The A chains have phospholipase A2 activity and the B chains show
homology with the basic protease inhibitors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: Y12100; CAA72809.1; -.
DR HSSP: P00981; IDTK.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Toxin; Neurotoxin; Presynaptic neurotoxin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 85
FT DOMAIN 31 81 BETA BUNGAROTOXIN B1 CHAIN, MAJOR
FT DISULFID 31 81 COMPONENT.
FT DISULFID 40 64 BPTI/KUNITZ INHIBITOR.
FT DISULFID 56 77 BY SIMILARITY.
FT DISULFID 79 79 BY SIMILARITY.
FT ACT SITE 41 42 INTERCHAIN (WITH AN A CHAIN).
FT MUTAGEN 79 79 REACTIVE BOND (BY SIMILARITY).
FT C-8; LOSS OF PA2 ACTIVITY. WEAK LOSS IN
FT FOLDING.
FT CONFLICT 45 45 MISSING (IN REF. 2).
FT CONFLICT 65 70 NONGEN -> DEDDEN (IN REF. 2).
SQ SEQUENCE 85 AA; 9571 MW; A1E3D452A67DE5C CRC64;

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DR PRINTS; PR00759; BASICPTAB.
DR Prodom; PD000222; Kuntz BPTI; 1..

DR SMART; SMO0131; KU; 1.
 DR SMART; SMO0217; WAP; 1.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor; Pyrolydine carboxylic acid.
 FT DOMAIN 8 58 BPTI/KUNITZ INHIBITOR.
 FT MOD_RES 63 105 WAP.
 FT DISULFID 1 1 PYROLYDINE CARBOXYLIC ACID.
 FT DISULFID 17 58 BY SIMILARITY.
 FT DISULFID 33 41 BY SIMILARITY.
 FT DISULFID 67 92 BY SIMILARITY.
 FT DISULFID 76 97 BY SIMILARITY.
 FT DISULFID 80 93 BY SIMILARITY.
 FT DISULFID 86 101 BY SIMILARITY.
 FT ACT_SITE 18 19 REACTIVE BOND (TRYPSIN).
 SQ SEQUENCE 110 AA; 11916 MW; 2694362438134188 CRC64;
 Query Match 41.4%; Score 189; DB 1; Length 110;
 Best Local Similarity 53.6%; Pred. No. 8.4e-15;
 Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 QY 26 DRDPFCELPADTGPCRVFPSPFTYNPDEKCLPFGCCBGNANFTKECESTC 81
 Db 3 DKRDICRLPFGPCGKGRIPRYFYNPASRMCESPFYGGCKGNKNNFKTKACGVRA 58
 RESULT 12
 TFP2 MOUSE STANDARD; PRT; 230 AA.
 ID TFP2 MOUSE STANDARD; PRT; 230 AA.
 AC 03536;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tissue factor pathway inhibitor 2 precursor (TFPI-2).
 GN TFPI2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97101108; PubMed=8945635;
 RA Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,
 Itoh H., Hori T., Aoki I., Miugui K., Miyazaki K.;
 RT "Cloning of the cDNA encoding mouse PPS/TFPI-2 and mapping of the gene
 to chromosome 6.";
 RT DNA Cell Biol. 15:947-954(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=20132652; PubMed=10669168;
 RA Kazama Y., Kamei S., Kuiper J.L., Foster D.C., Klei W.;
 RT "Nucleotide sequence of the gene encoding murine tissue factor pathway
 inhibitor-2.";
 RT Thromb. Haemost. 83:141-147(2000).
 RL [1]
 CC -1- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
 WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA. ALSO EXPRESSED
 IN LIVER AND KIDNEY.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- SWITLAKITY: Contains 3 BPTI/Kunitz inhibitor domains.
 CC -----
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announcel/
 CC or send an email to license@isb-sib.ch).

CC EMBL; D50586; BA22585.1;
 DR EMBL; AF180353; AAF40412.1;
 DR HSPB; P12111; IKT.
 DR MSD; MG1:108543; Tfp12.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 2.
 DR SMART; SMO0131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
 KM Serine protease inhibitor; Glycoprotein; Repeat; Signal;
 FT Blood coagulation.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 230 TISSUE FACTOR PATHWAY INHIBITOR 2.
 FT DOMAIN 36 86 BPTI/KUNITZ INHIBITOR 1.
 FT DOMAIN 96 146 BPTI/KUNITZ INHIBITOR 2.
 FT DOMAIN 156 206 BPTI/KUNITZ INHIBITOR 3.
 FT ACT_SITE 46 47 REACTIVE BOND (BY SIMILARITY).
 FT ACT_SITE 106 107 REACTIVE BOND (BY SIMILARITY).
 FT ACT_SITE 166 167 REACTIVE BOND (BY SIMILARITY).
 FT ACT_SITE 166 167 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 36 86 BY SIMILARITY.
 FT DISULFID 45 69 BY SIMILARITY.
 FT DISULFID 61 82 BY SIMILARITY.
 FT DISULFID 96 146 BY SIMILARITY.
 FT DISULFID 105 129 BY SIMILARITY.
 FT DISULFID 121 142 BY SIMILARITY.
 FT DISULFID 156 206 BY SIMILARITY.
 FT DISULFID 165 189 BY SIMILARITY.
 FT DISULFID 181 202 BY SIMILARITY.
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 230 AA; 26137 MW; 57EAD2E36521C7B CRC64;
 Query Match 41.2%; Score 188.5; DB 1; Length 230;
 Best Local Similarity 42.7%; Pred. No. 2.1e-14;
 Matches 35; Conservative 14; Mismatches 22; Indels 11; Gaps 2;
 QY 13 LTWMEV-----LTPVSK-DRDPFCELPADTGPCRVFPSPFTYNPDEKCLPFG 61
 Db 7 LQNLNPLLVGVSVGLTSVSAQGNLLEICLLPDAGFCQALLPFTYDRDQCKRRFY 66
 QY 62 GCEGNANFTKESCESTCA 83
 Db 67 GCGGNANFTSRDLCCOTCS 88
 RESULT 13
 ISIK HELPO STANDARD; PRT; 58 AA.
 ID ISIK HELPO STANDARD; PRT; 58 AA.
 AC P00954;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor K.
 OS Helix pomatia (Roman snail) (Edible snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
 OC Sigmurethra; Helicoidea; Helicidae; Helix.
 OX NCBI_TaxID=6536;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=76043680; PubMed=1183446;
 RX Technische H., Dietl T.;
 RA "The amino-acid sequence of isoform K form snails (Helix
 pomatia). A sequence determination by automated Edman degradation and
 RT mass-spectral identification of the phenylthiohydantoin.";
 RL Eur. J. Biochem. 58:439-451(1975).
 RL [2]
 RN DISULFIDE BONDS.
 RP MEDLINE=76143310; PubMed=3462;
 RA Dietl T., Technische H.;
 RT "The disulfide bridges of the trypsin-kallikrein inhibitor K from

RT snails (Helix pomatia). Thermal inactivation and proteolysis by
 RT chemoelysin."
 RL Hope-Sealyer's Z. Physiol. Chem. 357:139-145(1976).
 CC -1- FUNCTION: THIS IS ONE OF SEVERAL ISOINHIBITORS OF BROAD
 CC SPECIFICITY THAT ARE SECRETED INTO THE MUCUS OF THE SNAIL.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: A91232; TIRAB.
 DR HSP: P00974; 1BPI.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT_SITE 17 18
 SQ SEQUENCE 58 AA; 6451 MW; 6796586C488453B7 CRC64;
 Query Match 41.1%; Score 188; DB 1; Length 58;
 Best Local Similarity 52.7%; Pred. No. 5,6e-15;
 Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 QY 27 RDPCELPADNPGRCRFRPSFYNNPDKKLEFLYGGCGEGNANPFTKEGCESTC 81
 DB 3 RSPFCNLPAGTGPCKASFRYYNNSKSGGQOPFYGGCGRNQNRFTYOCQGV 57
 RESULT 14
 CSTI_BOMMO STANDARD; PRT; 55 AA.
 AC P81902;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxId=7091;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=Asahi;
 RX MEDLINE=99115431; PubMed=9914483;
 RA Kurooka A., Yamazaki M., Hirano H.;
 RT "Primary structure and possible functions of a trypsin inhibitor of
 RT Bombyx mori";
 RL Eur. J. Biochem. 259:120-126(1999).
 CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
 CC Activity by forming a low-dissociation complex with trypsin. May
 CC play an important part in regulating proteolytic activity in the
 CC silk gland or protecting silk proteins from degradation during
 CC histolysis.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
 CC gland.
 CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
 CC middle silk glands during the final stage of larval growth with
 CC highest expression before the onset of spinning.
 CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
 CC -1- MISCELLANEOUS: Has an isoelectric point of 4.3.
 CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR HSP: P31713; 1SHF.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTAS.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Developmental protein; Serine protease inhibitor.
 FT DISULFID 4 54
 FT DISULFID 13 37
 FT DISULFID 29 50
 FT ACT_SITE 14 15
 SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2BBE59 CRC64;
 Query Match 41.0%; Score 187.5; DB 1; Length 55;
 Best Local Similarity 61.1%; Pred. No. 6,1e-15;
 Matches 33; Conservative 6; Mismatches 14; Indels 1; Gaps 1;
 QY 28 PDPCELPADNPGRCRFRPSFYNNPDKKLEFLYGGCGEGNANPFTKEGCESTC 81
 DB 2 PDPCELPADNPGRCRFRPSFYNNPDKKLEFLYGGCGEGNANPFTKEGCESTC 81
 RESULT 15
 SPT2_HUMAN STANDARD; PRT; 252 AA.
 AC Q43251; O00271; O14895; Q969E0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kunitz-type protease inhibitor 2 precursor (Hepaticocyte growth factor
 DE activator inhibitor type 2) (HAI-2) (Placental bikunin).
 GN SPTN2 OR HAI2 OR KOP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98010584; PubMed=9346890;
 RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
 RA Kitamura N.;
 RT "Purification and cloning of hepaticocyte growth factor activator
 RT inhibitor type 2, a Kunitz-type serine protease inhibitor";
 RL J. Biol. Chem. 272:27558-27564(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC TISSUE=Placenta;
 RX MEDLINE=9227372; PubMed=9115294;
 RA Warior C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
 RA Tamburini P.P.;
 RT "Identification, and cloning of human placental bikunin, a novel serine
 RT protease inhibitor containing two Kunitz domains";
 RL J. Biol. Chem. 272:12202-12208(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancereatic cancer;
 RX MEDLINE=98094245; PubMed=9434156;
 RA Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friese H.,
 RA Buechler M., Adler G., Gress T.M.;
 RT "Cloning of a new Kunitz-type protease inhibitor with a putative
 RT transmembrane domain overexpressed in pancreatic cancer";
 RL Biochim. Biophys. Acta 1395:88-95(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT LEU-200.
 RC TISSUE=Colon, and Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin C.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters S.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,
 CC PLASMA AND TISSUE KALIKREIN, AND FACTOR XIA.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,
 CC PROSTATE, TESTIS, THYMUS, AND TRACHEA.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB006534; BAA25024.1; -.
 DR EMBL; U78095; AAC02781.1; -.
 DR EMBL; AF027205; AAB84031.1; -.
 DR EMBL; BC001668; AAH07705.1; -.
 DR EMBL; BC007705; AAH07705.1; -.
 DR EMBL; BC011951; AAH11951.1; -.
 DR EMBL; BC011955; AAH11955.1; -.
 DR EMBL; BC012868; AAH12868.1; -.
 DR HSSP; P05067; IAAI.
 DR GeneW; HGNC:11247; SPINT2.
 DR MIM; 605124; -.
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0004867; F:serine protease inhibitor activity; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR PRINTS; PR00759; BASICTPASE.
 DR PRODom; PD000222; Kunitz_BPTI; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
 DR Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
 KW Signal; Polymorphism.
 FT SIGNAL 1 27
 FT CHAIN 28 252
 FT DOMAIN 28 197
 FT TRANSMEM 198 218
 FT DOMAIN 219 252
 FT DOMAIN 38 88
 FT DOMAIN 133 183
 FT DISULFID 38 88
 FT DISULFID 47 71
 FT DISULFID 63 84
 FT ACT SITE 48 49
 FT DISULFID 133 183
 FT DISULFID 142 166
 FT DISULFID 158 179
 FT ACT SITE 143 144
 FT CARBOHYD 57 57
 FT CARBOHYD 94 94
 FT VARIANT 200 200
 FT CONFLICT 3 3
 FT CONFLICT 11 11
 FT CONFLICT 53 53
 /FTid=VAR_012482.
 Q -> H (IN REF. 3).
 R -> P (IN REF. 1).
 R -> K (IN REF. 3).

FT CONFLICT 240 240 D -> H (IN REF. 3).
 SQ SEQUENCE 252 AA; 28228 MW; A7D336DC0ECB2B CRC64;
 Query Match 39.4%; Score 180; DB 1; Length 252;
 Best Local Similarity 43.8%; Pred. No. 2.1e-13;
 Matches 35; Conservative 10; Mismatches 35; Indels 0; Gaps 0;
 Qy 3 SGGILLLLGLITLMEVLTVPVSSKDRPDPCELPADTGPCRVRFPSFYNNPDEKCKLEPIYG 62
 Db 10 SRAFLALLSGSLISGLVLAADRESRSHDFCLVSKVGRCRASMPRWYNTVDGSCOLFVYG 69
 Qy 63 GCEGANNNFTYKEECSTCA 82
 Db 70 GCDGNNNNYLTKEECLKCA 89

Search completed: January 23, 2004, 10:25:15
 Job time : 8.59859 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 31.2711 Seconds
(without alignments)
664.925 Million cell updates/sec

Title: US-09-700-179A-16

Sequence: 1 MSSGGLLLGLTWLVLT.....CEGNANFTYKCESTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seges, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvirts:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	457	100.0	83	13	Q90WA1
2	438	95.8	83	13	Q90WA0
3	361	79.0	83	13	Q90W99
4	357	78.1	83	13	Q90W98
5	357	78.1	83	13	Q90W96
6	342	74.8	83	13	Q90W97
7	293	64.1	88	13	Q8AY43
8	287	62.8	88	13	Q8AY41
9	277	60.6	88	13	Q8AY42
10	248	54.3	90	13	Q8AY44
11	241	52.7	90	13	Q8AY45
12	239	52.3	79	13	Q91351
13	201	44.0	90	13	Q8AY46
14	198	43.3	58	5	Q9TWP9
15	194	42.5	85	13	Q9PTA4
16	190	41.6	59	5	Q9TWP8

17	190	41.6	85	13	Q9W728	Q9W728 bungarus mu
18	187.5	41.0	76	5	Q8T7L9	Q8T7L9 bombyx mori
19	187.5	41.0	230	11	Q8CF99	Q8CF99 rattus norv
20	185	40.5	58	5	Q9TWG0	Q9TWG0 anemonia su
21	185	40.5	86	5	Q9GPI5	Q9GPI5 ixodes ricci
22	184.5	40.4	80	5	Q8T357	Q8T357 araneus ven
23	181	39.6	984	5	Q9GQNZ	Q9GQNZ callactis
24	181	39.6	984	5	Q9GQNZ	Q9GQNZ callactis
25	179	39.2	142	5	Q8WP12	Q8WP12 boophilus m
26	176.5	38.6	142	5	Q8WP13	Q8WP13 boophilus m
27	173	37.9	113	5	Q9V508	Q9V508 drosophila
28	172	37.6	759	5	Q8T191	Q8T191 ancylostoma
29	171.5	37.5	57	5	Q8MTR6	Q8MTR6 haematobia
30	171	37.4	235	11	Q8C180	Q8C180 mus musculu
31	171	37.4	235	11	Q8C180	Q8C180 mus musculu
32	169	37.0	396	6	Q28874	Q28874 canis famli
33	167.5	36.7	82	5	Q8MVB4	Q8MVB4 ixodes scap
34	165.5	36.2	1572	5	Q44938	Q44938 haemochus
35	164	35.9	132	5	Q9VQ79	Q9VQ79 haemochus
36	163	35.7	195	11	Q9D8Q8	Q9D8Q8 mus musculu
37	161	35.2	548	4	Q96NZ8	Q96NZ8 mus sapien
38	161	35.2	576	4	Q8TEU8	Q8TEU8 homo sapien
39	161	35.2	3198	5	Q9UGG8	Q9UGG8 manduca sex
40	160.5	35.1	224	4	Q8NAX6	Q8NAX6 homo sapien
41	160	35.0	979	4	Q8NAZ1	Q8NAZ1 homo sapien
42	159	34.8	85	5	Q8WP15	Q8WP15 bombyx mori
43	158	34.6	76	5	Q968S8	Q968S8 galliera me
44	158	34.6	169	6	Q9NOX7	Q9NOX7 bos taurus
45	158	34.6	461	5	Q95822	Q95822 drosophila

ALIGNMENTS

RESULT 1

ID	Q90WA1	PRELIMINARY	PRT	83 AA.
AC	Q90WA1			
DT	01-DEC-2001 (TEMBREL. 19, Created)			
DT	01-DEC-2001 (TEMBREL. 19, Last sequence update)			
DT	01-MAR-2003 (TEMBREL. 23, Last annotation update)			
DE	Textilis			
OS	Pseudonaja textilis textilis.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Rhaphidia; Acanthophinae; Pseudonaja.			
OX	NCBI_TaxID=169397;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Macci P.P., Layvin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;			
RT	"Plasma inhibitors from the Australian brown snake Pseudonaja			
RT	textilis textilis.";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Venom gland;			
RA	Filipovich I.V., Sorokina N.I., Macci P.P., de Jersey J.,			
RA	Whitaker A.N., Gaffney P.J., Layvin M.F.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF402324; AAK9519.1; -			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI; 1.			
DR	ProDom; PD000222; Kunitz_BPTI; 1.			
DR	SMART; SM00131; KUT; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Protease inhibitor; Serine protease inhibitor.			
SQ	SEQUENCE 83 AA; 9173 MW; 2045850657014221 CRC64;			

Query Match 100.0%; Score 457; DB 13; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSGGLLLGLTLTMEVLPVSSKDRPDPFCELPADPGCRVRRPSPFYNPDEKCKLEFI 60
 DB 1 MSSGGLLLGLTLTMEVLPVSSKDRPDPFCELPADPGCRVRRPSPFYNPDEKCKLEFI 60
 QY 61 YGCGEGNANNPTKECESTCA 83
 DB 61 YGCGEGNANNPTKECESTCA 83

RESULT 2

Q90WA0 PRELIMINARY; PRT; 83 AA.
 AC Q90WA0;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Textilinin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophinae; Pseudonaja.
 OC NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402325; AAK95520.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.
 DR ProDom; PD000222; Kunitz_BPTI.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9179 MW; 67859AD27175930 CRC64;
 Query Match 95.8%; Score 438; DB 13; Length 83;
 Best Local Similarity 95.2%; Pred. No. 4.6e-47;
 Matches 79; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MSSGGLLLGLTLTMEVLPVSSKDRPDPFCELPADPGCRVRRPSPFYNPDEKCKLEFI 60
 DB 1 MSSGGLLLGLTLTMEVLPVSSKDRPDPFCELPADPGCRVRRPSPFYNPDEKCKLEFI 60
 QY 61 YGCGEGNANNPTKECESTCA 83
 DB 61 YGCGEGNANNPTKECESTCA 83

RESULT 3

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Textilinin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophinae; Pseudonaja.
 OC NCBI_TaxID=169397;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402326; AAK95521.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.
 DR ProDom; PD000222; Kunitz_BPTI.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9158 MW; 368E82487ACFB61 CRC64;
 Query Match 79.0%; Score 361; DB 13; Length 83;
 Best Local Similarity 77.1%; Pred. No. 2e-37;
 Matches 64; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MSSGGLLLGLTLTMEVLPVSSKDRPDPFCELPADPGCRVRRPSPFYNPDEKCKLEFI 60
 DB 1 MSSGGLLLGLTLTMEVLPVSSKDRPDPFCELPADPGCRVRRPSPFYNPDEKCKLEFI 60
 QY 61 YGCGEGNANNPTKECESTCA 83
 DB 61 YGCGEGNANNPTKECESTCA 83

RESULT 4

Q90W98 PRELIMINARY; PRT; 83 AA.
 AC Q90W98;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Textilinin.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acantophinae; Pseudonaja.
 OC NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402327; AAK95522.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI.
 DR ProDom; PD000222; Kunitz_BPTI.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 8983 MW; 3F28548146848A9B CRC64;
 Query Match 78.1%; Score 357; DB 13; Length 83;
 Best Local Similarity 79.5%; Pred. No. 6.2e-37;

Matches 66; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60
 DB 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60

QY 61 YGCGGANNPITKECESTCA 83
 DB 61 YGCGGANNPITKECESTCA 83

RESULT 5

ID Q90W96 PRELIMINARY; PRT; 83 AA.

AC Q90W96; 090W96;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Textillinin.

OS Pseudonaja textilis textilis.

OC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.

OX NCBI_TaxID=169397;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA Masci P.P., Lavlin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis.";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RL Whitaker A.N., Gaffney P.J., Lavlin M.F.,
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF402329; AAK95348.1; -
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASB.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.

SQ SEQUENCE 83 AA; 9060 MW; A60DF2692864C58E CRC64;

Query Match 78.1%; Score 357; DB 13; Length 83;
 Best Local Similarity 79.5%; Pred. No. 6.2e-37;
 Matches 66; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60
 DB 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60

QY 61 YGCGGANNPITKECESTCA 83
 DB 61 YGCGGANNPITKECESTCA 83

RESULT 6

ID Q90W97 PRELIMINARY; PRT; 83 AA.

AC Q90W97; 090W97;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Textillinin.

OS Pseudonaja textilis textilis.

OC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.

OX NCBI_TaxID=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavlin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.,
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis.";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA Filipovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
 RL Whitaker A.N., Gaffney P.J., Lavlin M.F.,
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF402328; AAK95523.1; -
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.

SQ SEQUENCE 83 AA; 9031 MW; 9CAA7FE390D9B191 CRC64;

Query Match 74.8%; Score 342; DB 13; Length 83;
 Best Local Similarity 77.1%; Pred. No. 4.7e-35;
 Matches 64; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60
 DB 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60

QY 61 YGCGGANNPITKECESTCA 83
 DB 61 YGCGGANNPITKECESTCA 83

RESULT 7

ID Q8AY43 PRELIMINARY; PRT; 88 AA.

AC Q8AY43; 08AY43;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Kunitz inhibitor a (Fragment).

OS Bungarus candidus (Malayan Krait).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.

OX NCBI_TaxID=92438;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA Teal I.H., Wang Y.M., Hsu H.Y.,
 RT "Structural and functional genomics of Bungarus candidus.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY057886; AAL30068.1; -
 DR NON TER 1
 FT 1

SQ SEQUENCE 88 AA; 9606 MW; E2C089906909563D CRC64;

Query Match 64.1%; Score 293; DB 13; Length 88;
 Best Local Similarity 65.9%; Pred. No. 6.7e-29;
 Matches 54; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 60
 DB 6 MSSGGLLLLGLTLTMEVLTTPVSSKDRPDPFCGLPADTGPCRVRRPSPFYNDKKCLEFI 65

QY 61 YGCGGANNPITKECESTCA 82
 DB 66 YGCGGANNPITKECESTCA 87

RESULT 8

08AY41 PRELIMINARY: PRT; 88 AA.
AC 08AY41;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kunitz inhibitor c (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057885; AAL30070.1; --
FT NON TER 1
SQ SEQUENCE 88 AA; 9659 MW; 0279950755F6B787 CRC64;
Query Match 62.8%; Score 287; DB 13; Length 88;
Best Local Similarity 67.1%; Pred. No. 3.8e-28;
Matches 55; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
QY 1 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKCESTC 82
DB 66 YGCGGNANPFTKCESTC 87

RESULT 9

08AY42 PRELIMINARY: PRT; 88 AA.
AC 08AY42;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kunitz inhibitor b (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057887; AAL30069.1; --
FT NON TER 1
SQ SEQUENCE 88 AA; 9391 MW; 71F9P57D36E7A652 CRC64;
Query Match 60.6%; Score 277; DB 13; Length 88;
Best Local Similarity 63.0%; Pred. No. 6.7e-27;
Matches 51; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
QY 1 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKCESTC 81
DB 66 YGCGGNANPFTKCESTC 86

RESULT 10

08AY44 PRELIMINARY: PRT; 90 AA.
AC 08AY44;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta bungarotoxin B2b chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057885; AAL30067.1; --
FT NON TER 1
SQ SEQUENCE 90 AA; 10281 MW; 15754C179BDE190B CRC64;
Query Match 54.3%; Score 248; DB 13; Length 90;
Best Local Similarity 56.8%; Pred. No. 2.9e-23;
Matches 46; Conservative 10; Mismatches 25; Indels 0; Gaps 0;
QY 1 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKCESTC 81
DB 66 YGCGGNANPFTKCESTC 86

RESULT 11

08AY45 PRELIMINARY: PRT; 90 AA.
AC 08AY45;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta bungarotoxin B2a chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057884; AAL30066.1; --
FT NON TER 1
SQ SEQUENCE 90 AA; 10122 MW; AD0FBE279D68A910 CRC64;
Query Match 52.7%; Score 241; DB 13; Length 90;
Best Local Similarity 55.6%; Pred. No. 2.2e-22;
Matches 45; Conservative 9; Mismatches 27; Indels 0; Gaps 0;
QY 1 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 60
DB 6 MSSGILLILGLITLMEVITPVSSKDRPDPFCPLPADTGRCVRFPSPFYNNPDEKCLEFI 65
QY 61 YGCGGNANPFTKCESTC 81
DB 66 YGCGGNANPFTKCESTC 86

RESULT 12

091351


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ID 091351 PRELIMINARY; PRT; 79 AA.
AC 091351;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Dendrotoxin K (Fragment).
GN DENDROTOXIN K, DTXK.
OS Dendroaspis polyLepis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OC NCBI_TaxId=8624;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277850; PubMed=8504088;
RA Smith L.A., Lafaye P.J., Lapentotiere H.F., Spain T., Dolly J.O.;
RT "Cloning and functional expression of dendrotoxin K from black mamba,
a K+ channel blocker.";
RL Biochemistry 32:5692-5697(1993).
DR EMBL; S61886; AAB26988.1; -.
DR HSSP; P00981; IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
FT NON TER 1
SQ SEQUENCE 79 AA; 8851 MW; DCDP89AFA07D7D46 CRC64;

Query Match 52.3%; Score 239; DB 13; Length 79;
Best Local Similarity 59.5%; Pred. No. 3.4e-22;
Matches 47; Conservative 6; Mismatches 24; Indels 2; Gaps 1;

QY 3 SGGILLILGLTLTWBVLTPVSSKDRDPCELPADTPGCRVRFPSFYNNPDEKCKLEFIYG 62
DB 1 SGGILLILGLTLTWBVLTPVSSKDRDPCELPADTPGCRVRFPSFYNNPDEKCKLEFIYG 62
DB 59 GCGGNANPFITKECESTC 81
DB 59 GCGGNANPFITKECESTC 77

RESULT 13
ID 08AY46 PRELIMINARY; PRT; 90 AA.
AC 08AY46;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Beta bungarotoxin BI chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCBI_TaxId=92438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tsai I.H., Wang Y.M., Hsu H.Y.;
RT "Structural and functional genomics of Bungarus candidus.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBD databases.
DR EMBL; AY057883; AAL30065.1; -.
FT NON TER 1
SQ SEQUENCE 90 AA; 10048 MW; E05C2A0D28179726 CRC64;

Query Match 44.0%; Score 201; DB 13; Length 90;
Best Local Similarity 53.1%; Pred. No. 2.2e-17;
Matches 43; Conservative 6; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSSGILLILGLTLTWBVLTPVSSKDRDPCELPADTPGCRVRFPSFYNNPDEKCKLEFI 60

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DB 6 MSSGILLILGLTLTWBVLTPVSSKDRDPCELPADTPGCRVRFPSFYNNPDEKCKLEFI 65
QY 61 YGCGGNANPFITKECESTC 81
DB 66 YGCGGNANPFITKECESTC 86

RESULT 14
ID 09TFP9 PRELIMINARY; PRT; 58 AA.
AC 09TFP9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE KALITUDINE 2, ASK2.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Scleractinia; Actinoptera;
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Scleractinia; Actinoptera;
OC NCB1_TaxId=6108;
RN [1]
RP SEQUENCE.
RX MEDLINE=96027617; PubMed=7559645;
RA Schwelb H., Bruhn T., Guilleme E., Moliner D., Lancelin J.M.,
RA Beres L., Lazdunski M.;
RT "Kalicludines and kalipeptine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels.";
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSSP; P12111; 2KNT.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6778 MW; P102E71682F1A55C CRC64;

Query Match 43.3%; Score 198; DB 5; Length 58;
Best Local Similarity 62.7%; Pred. No. 3.3e-17;
Matches 32; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 31 CELPADTPGCRVRFPSFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 81
DB 5 CELPADTPGCRVRFPSFYNNPDEKCKLEFIYGCCEGNANPFITKECESTC 81

RESULT 15
ID 09PTA4 PRELIMINARY; PRT; 85 AA.
AC 09PTA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Beta-bungarotoxin BI precursor.
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCBI_TaxId=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wu P.F., Chang L.S.;
RT "Genetic structures of A chain and B chain of beta-bungarotoxin from
RT Taiwan banded krait (Bungarus multicinctus). A chain genes and B chain
genes do not share a common origin.";
RL Eur. J. Biochem. 267:4668-4675(2000).
DR EMBL; AJ251223; CAB62503.1; -.
DR HSSP; P00981; IDTK.

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DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor; signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 1 85 BETA-BUNGAROTOXIN B1.
 SQ SEQUENCE 85 AA; 9555 MW; BSA78452AE7CC55C CRC64;

Query Match. 42.5%; Score 194; DB 13; Length 85;
 Best Local Similarity 51.9%; Pred. No. 1.6e-16;
 Matches 42; Conservative 6; Mismatches 33; Indels 0; Gaps 0;

QY	1	MSSGGLLLLLGLTLTMEVLTVPVSSKDRPDPFCELPADTPGCRVRFPSFYINPEKKCLEFI	60
DB	1	MSSGGLLLLLGLTLTSAELIPVSSRQRHRDCDKPPKNGCGVRRDAFYDTRLKTKCAEQ	60
QY	61	YGCCEGNANNFITKECESTC	81
DB	61	YRGCGNGNHRPTETLCRCGC	81

Search completed: January 23, 2004, 10:27:16
 Job time : 31.2711 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 23, 2004, 10:21:23 ; Search time 12.8592 Seconds
(without alignments)
620.725 Million cell updates/sec

Title: US-09-700-179a-16

Sequence: 1 MSSGGLLLGLLTLEWVLT.....CEGNANPFITKECESTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	239	52.3	79	1	TIBPVK K+ channel blocker
2	217	47.5	62	2	taicatoxin serine
3	214	46.8	65	1	venom basic protei
4	204	44.6	62	2	protease inhibitor
5	201	44.0	57	1	venom basic protei
6	201	44.0	61	1	venom basic protei
7	198	43.3	57	1	venom basic protei
8	195	42.7	62	2	venom basic protei
9	194	42.5	57	2	venom animal Kunlt
10	189	41.4	110	1	basic protease i
11	188	41.1	58	1	iso inhibitor K (BP
12	179	39.2	57	2	short epsilon-dend
13	179	39.2	59	1	venom basic protei
14	179	39.2	59	1	Long epsilon-dendr
15	178	38.9	60	1	venom basic protei
16	172	37.6	302	1	venom basic protei
17	171.5	37.5	299	2	venom basic protei
18	171	37.4	300	2	venom basic protei
19	170.5	37.3	122	1	lipoprotein-associ
20	170	37.2	235	1	uterine plasmin/er
21	169	37.0	57	1	venom basic protei
22	169	37.0	304	1	venom basic protei
23	169	37.0	396	2	venom basic protei
24	167	36.5	57	2	basic protease i
25	166.5	36.4	100	1	basic protease i
26	165	35.8	57	1	protease inhibitor
27	163.5	35.7	252	2	spleen basic prote
28	163	35.4	304	1	hepatocyte growth
29	162	35.4	304	1	venom basic protei

ALIGNMENTS

RESULT 1

TIBPVK K+ channel blocker dendrotoxin K - black mamba

C:Species: Dendroaspis polylepsis polylepsis (black mamba)
C>Date: 30-Nov-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

C:Accession: A49291; A01213
R:Smith, L.A.; Lafaye, P.J.; Lapenotiere, H.F.; Spain, T.; Dolly, J.O.

Biochemistry 32, 5692-5697, 1993
A:Title: Cloning and functional expression of dendrotoxin K from black mamba, a K+ char

A:Reference number: A49291; PMID:93277850; PMID:8504088
A:Accession: A49291

A:Status: preliminary
A:Molecule type: mRNA; protein

A:Residues: 1-79 <SWT>
A:Cross-References: GB:56186; NID:9385317; PID:9385318

A:Note: sequence extracted from NCBI database (NCBI:133053, NCBI:133054)
A:Note: the source is designated as Dendroaspis polylepsis

R:Stridom, D.J.
Biochim. Biophys. Acta 491, 361-369, 1977

A:Title: Snake venom toxins. The amino acid sequence of toxin Vi2, a homologue of pancr

A:Reference number: A90617; PMID:77158065; PMID:857902
A:Accession: A01213

A:Molecule type: protein
A:Residues: 23-79 <SWT>

C:Comment: This protein is much less toxic to mice than is whole venom. It inhibits try

C:Superfamily: basic protease inhibitor; animal Kunitz-type protease inhibitor hom

C:Keywords: serine protease inhibitor; venom
F:27-77/Domain: animal Kunitz-type protease inhibitor homology <BPI>

F:27-77,36-60,52-73/Disulfide bonds: #status predicted

Query Match 52.3%; Score 239; DB 1; Length 79;
Best Local Similarity 59.5%; Pred. No. 8.7e-19;

Matches 47; Conservative 6; Mismatches 24; Indels 2; Gaps 1;

QY	3	SGGILLGLLTLEWVLT	PPVSSKDPCEPADTGPCRVFPFFSYNPDEKCLEFTYG	62
DB	1	SGHLLMLGLLTLEWVLT	PPVSSGAAK--YCKPLPIGPKRKIPSYTYMKKKKQCLPFDYS	58
QY	63	GCEGNANPFITKECESTC	81	
DB	59	GCGGNANPFITKECESTC	77	

RESULT 2

A44180 taicatoxin serine protease inhibitor component - Australian taipan

C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C:Accession: A44180
R:Posanti, L.D.; Martin, B.M.; Yatani, A.; Mochizuki, J.; Zamudio, F.Z.; Gurrola,

Toxicol 30, 1343-1364, 1992
A:Title: Isolation and physiological characterization of taicatoxin, a complex toxin w

A:Reference number: A44180; MUID:93134601; PMID:1485334

A:Accession: A44180

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-62 <POS>

A:Experimental source: subsp. scutellatus, venom

A>Note: sequence extracted from NCBI backbone (NCBI:P122482)

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor

F:1-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.5%; Score 217; DB 2; Length 62;

Best Local Similarity 63.2%; Pred. No. 1.6e-16;

Matches 36; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 25 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 81

Db 1 RDRPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 57

RESULT 3
TITVVC

venom basic proteinase inhibitor III - sand viper

N:Alternate names: venom chymotrypsin inhibitor

C:Species: Viper aamodytes (sand viper)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #ext_change 16-Aug-1996

C:Accession: A01223

R:Ritonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 746, 138-145, 1983

A>Title: The primary structure Of Viper aamodytes venom chymotrypsin inhibitor.

A:Reference number: A01223

A:Accession: A01223

A:Molecule type: protein

A:Residues: 1-65 <RT>

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor; venom

F:1-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:1-57,16-40,32-53/Diulfide bonds: #status predicted

F:17/inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 46.8%; Score 214; DB 1; Length 65;

Best Local Similarity 62.7%; Pred. No. 3.5e-16;

Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 83

Db 1 RDRPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 59

RESULT 4

S07451

proteinase inhibitor 5. II - snake-locks sea anemone

C:Species: Anemone sulcata (snake-locks sea anemone)

C>Date: 31-Dec-1990 #sequence_revision 09-May-1997 #ext_change 09-May-1997

C:Accession: S07451; B27222

R:Munderer, G.; Machleidt, W.; Filtz, H.

Meth. Enzymol. 80, 816-820, 1981

A>Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemone

A:Reference number: S07451

A:Accession: S07451

A:Molecule type: protein

A:Residues: 1-59 <WUN>

A>Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found

R:Krebs, H.C.; Habermehl, G.G.

Naturwissenschaften 74, 395-396, 1987

A>Title: Isolierung und strukturaufklärung eines haemolytisch aktiven peptids aus der

A:Reference number: A94700

A:Accession: B27222

A:Molecule type: protein

A:Residues: 1-38, 'R', '40', 'B', '42', 'BB', '45-48', 'ZZ', '51', 'Z', '53-62 <KRB>

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor

F:1-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 44.6%; Score 204; DB 2; Length 62;

Best Local Similarity 66.7%; Pred. No. 4e-15;

Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 31 CELPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 81

Db 5 CELPVYGCRRARFPFRYYNSSSKCKEFTYGGCGGNANFTTKECEKVC 55

RESULT 5

TINVC

venom basic proteinase inhibitor II - Cape cobra

C:Species: Naja naja (Cape cobra)

C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #ext_change 16-Aug-1996

C:Accession: A01217

R:Hoekema, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.

J. Biochem. 79, 559-578, 1976

A>Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibito

o acid sequences of two of them.

A:Reference number: A91942; MUID:76237547; PMID:950337

A:Accession: A01217

A:Molecule type: protein

A:Residues: 1-57 <HOK>

C:Comment: The activity of this inhibitor is probably similar to that of bovine basic

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C:Keywords: serine proteinase inhibitor; venom

F:1-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:1-55,14-38,30-51/Diulfide bonds: #status predicted

Query Match 44.0%; Score 201; DB 1; Length 57;

Best Local Similarity 63.6%; Pred. No. 7.6e-15;

Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 27 RDPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 81

Db 1 RDPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 55

RESULT 6

TITVTC

venom basic proteinase inhibitor I - western sand viper

N:Alternate names: venom trypsin inhibitor I

C:Species: Viper aamodytes aamodytes (western sand viper)

C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #ext_change 16-Aug-1996

C:Accession: A01222

R:Ritonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 746, 429-435, 1983

A>Title: The primary structure of Viper aamodytes venom trypsin inhibitor I.

A:Reference number: A01222; MUID:84053385; PMID:6639951

A:Accession: A01222

A:Molecule type: protein

A:Residues: 1-61 <RT>

C:Comment: This protein inhibits trypsin and kallikrein.

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C:Keywords: pyroglutamic acid; serine proteinase inhibitor; venom

F:1-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:1-57,16-40,32-53/Diulfide bonds: #status experimental

F:17/inhibitory site: Lys (trypsin) #status predicted

Query Match 44.0%; Score 201; DB 1; Length 61;

Best Local Similarity 57.6%; Pred. No. 8.2e-15;

Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 25 KDRPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 83

Db 1 DRPFCPLPADTGCRVRFPSFYNNPDEKCLLEFYGGCGGNANFTTKECESTC 59

RESULT 7

TITVTC

venom basic proteinase inhibitor II - ringhals

C/Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C/Accession: A01216
R/Hokama, Y.; Iwanaga, S.; Tateuchi, T.; Suzuki, T.
J. Biochem. 79, 559-578, 1976
A/Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
o acid sequences of two of them.
A/Reference number: A91942; MUID:76237547; PMID:950337
A/Accession: A01216
A/Molecule type: protein
A/Residues: 1-57 <HOK>
C/Comment: The activity of this inhibitor is similar to that of bovine basic proteinase in
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: serine proteinase inhibitor; venom
F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/5-55,14-38,30-51/Dissulfide bonds: #status predicted

Query Match 43.3%; Score 198; DB 1; Length 57;
Best Local Similarity 61.8%; Pred. No. 1.66-14;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 27 RPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 81
DB 1 RPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 55

RESULT 8

S19327
venom basic proteinase inhibitor - leaf-nosed viper

N/Alternate names: trypsin inhibitor (Kunitz-type)
C/Species: Eristicophis machaboni (leaf-nosed viper)

C/Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999

C/Accession: S19327
R/Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.

FEBS Lett. 294, 141-143, 1991

A/Title: Purification and characterization of a Kunitz-type trypsin inhibitor from leaf-
A/Reference number: S19327; MUID:92077130; PMID:1743283

A/Accession: S19327
A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-62 <SID>

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: serine proteinase inhibitor; venom

F/2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.7%; Score 195; DB 2; Length 62;
Best Local Similarity 61.1%; Pred. No. 3.7e-14;
Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTCA 83
DB 1 FCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTCA 54

RESULT 9
S13846
venom animal Kunitz-type trypsin inhibitor - Indian cobra

C/Species: Naja naja naja (Indian cobra)
C/Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000

C/Accession: S13846
R/Shafiq, J.; Beg, O.U.; Yln, S.J.; Zaidi, Z.H.; Joernvall, H.

Eur. J. Biochem. 194, 337-341, 1990

A/Title: Primary structure and functional properties of cobra (Naja naja) venom Kunitz-
A/Reference number: S13846; MUID:9109304; PMID:1702708

A/Accession: S13846
A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <SHA>

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: serine proteinase inhibitor; venom

F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.5%; Score 194; DB 2; Length 57;

Best Local Similarity 60.0%; Pred. No. 4.3e-14;
Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 27 RPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 81
DB 1 RPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 55

RESULT 10

TITROR
basic proteinase inhibitor - loggerhead

C/Species: Caretta caretta (loggerhead)

C/Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994

C/Accession: A01224
R/Kato, I.; Tomimaga, N.

Red. Proc. 38, 832, 1979

A/Title: Trypsin-subtilisin inhibitor from red sea turtle-eggwhite consists of two trypsin-
A/Reference number: A01224

A/Accession: A01224
A/Molecule type: protein

A/Residues: 1-110 <KAT>

C/Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain
C/Superfamily: loggthead basic proteinase inhibitor; animal Kunitz-type proteinase in
C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F/8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/63-105/Domain: antileukoproteinase repeat homology <ALP>

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8-58,17-41,33-54,67-93,76-97,80-92,86-101/Dissulfide bonds: #status predicted

Query Match 41.4%; Score 189; DB 1; Length 110;
Best Local Similarity 53.6%; Pred. No. 2.9e-13;
Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 26 DRPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 81
DB 3 DRPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 58

RESULT 11
TITROR
iso inhibitor K (BPI type) - Roman snail

C/Species: Helix pomatia (Roman snail)

C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994

C/Accession: A91232; A01225

R/Teschke, H.; Dietl, T.

Bur. J. Biochem. 58, 439-451, 1975

A/Title: The amino-acid sequence of iso inhibitor K from snails (Helix pomatia). A sequ
A/Reference number: A91232; MUID:76043680; PMID:1183446

A/Accession: A91232
A/Molecule type: protein

A/Residues: 1-58 <TSC>

R/Dietl, T.; Teschke, H.

Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976

A/Title: Die Disulfidbrücken des Trypsin-Kallikrein-Inhibitoren K aus Weinbergsschnecker
A/Reference number: A91666; MUID:76141310; PMID:3462

A/Contents: annotation; disulfide bonds

C/Comment: This is one of several iso inhibitors of broad specificity that are secreted
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/7-57,16-40,32-53/Dissulfide bonds: #status predicted

Query Match 41.1%; Score 188; DB 1; Length 58;
Best Local Similarity 52.7%; Pred. No. 1.9e-13;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 27 RPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 81
DB 3 RPDCELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANFRTKECESTC 57

RESULT 12

B59399

short epsilon-dendrotoxin H1a55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C:Accession: B59399

R:Sigle, R.; Hackett, M.; Alrd, S.D.

Toxicon 40, 297-308, 2002

A:Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis

A:Reference number: A59399

A:Accession: B59399

A:Status: Preliminary

A:Molecule type: protein

A:Note: trypsin inhibitor; K+ channel antagonist

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol

F:5-55/Disulfide bonds: #status experimental

F:14-38/Disulfide bonds: #status experimental

F:30-51/Disulfide bonds: #status experimental

Query Match 39.2%; Score 179; DB 2; Length 57;

Best Local Similarity 57.7%; Pred. No. 1.8e-12;

Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSFYNDPEKKCLEFTYGGCGGNANFTKECESTC 81

Db 4 FCKLPABPGPCAKSIPAFYNNMAKKCOLFHYGGCKGNANRSTIEKCRHAC 55

RESULT 13

TIPEPD

venom basic proteinase inhibitor B - black mamba

C:Species: Dendroaspis polylepsis polylepsis (black mamba)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01215

R:Joubert, P.J.; Strydom, D.J.

Eur. J. Biochem. 87, 191-198, 1978

A:Title: Snake venoms. The amino-acid sequence of trypsin inhibitor B of Dendroaspis pol

A:Reference number: A01215; MUID:78214615; PMID:668688

A:Accession: A01215

A:Molecule type: protein

A:Residues: 1-59 <JOU>

A:Note: this protein inhibits trypsin and binds transition metal ions such as copper and

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 39.2%; Score 179; DB 1; Length 59;

Best Local Similarity 57.7%; Pred. No. 1.8e-12;

Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSFYNDPEKKCLEFTYGGCGGNANFTKECESTC 81

Db 6 FCKLPABPGPCAKSIPAFYNNMAKKCOLFHYGGCKGNANRSTIEKCRHAC 57

RESULT 14

A59399

long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C:Accession: A59399

R:Sigle, R.; Hackett, M.; Alrd, S.D.

Toxicon 40, 297-308, 2002

A:Title: Primary structure of four dendrotoxin B homologs from the venom of Dendroaspis

A:Reference number: A59399

A:Accession: A59399

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-59 <AIR>

A:Note: trypsin inhibitor; K+ channel antagonist

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol

F:7-57/Disulfide bonds: #status experimental

F:16-40/Disulfide bonds: #status experimental

F:32-53/Disulfide bonds: #status experimental

Query Match 39.2%; Score 179; DB 2; Length 59;

Best Local Similarity 57.7%; Pred. No. 1.8e-12;

Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 30 FCELPADTGPCRVPRPSFYNDPEKKCLEFTYGGCGGNANFTKECESTC 81

Db 6 FCKLPABPGPCAKSIPAFYNNMAKKCOLFHYGGCKGNANRSTIEKCRHAC 57

RESULT 15

TIVRY2

venom basic proteinase inhibitor II - Russell's viper

C:Species: Vipera russelli (Russell's viper)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01221

R:Takahashi, H.; Iwanaga, S.; Kitagawa, T.; Hokama, Y.; Suzuki, T.

J. Biochem. 76, 721-733, 1974

A:Title: Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II iso

A:Reference number: A01221; MUID:75060360; PMID:4436285

A:Accession: A01221

A:Molecule type: protein

A:Note: This inhibitor has activity similar to that of bovine basic protease inhibi

C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor hom

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 38.9%; Score 178; DB 1; Length 60;

Best Local Similarity 53.6%; Pred. No. 2.4e-12;

Matches 30; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 26 DRPFCPLPADTGPCRVPRPSFYNDPEKKCLEFTYGGCGGNANFTKECESTC 81

Db 2 DRPFCPLPADTGPCRVPRPSFYNDPEKKCLEFTYGGCGGNANFTKECESTC 57

Search completed: January 23, 2004, 10:28:11

Job time : 13.8592 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:27:24 ; Search time 29.8099 Seconds
(without alignments)
575.620 Million cell updates/sec

Title: US-09-700-179a-16

Perfect score: 457
Sequence: 1 MSSGGILLGLTMEVLT.....CEGNANFTKEBCESTCA 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	221	48.4	58	12	US-10-038-722-5
2	214	46.8	62	12	US-10-038-722-110
3	214	46.8	62	12	US-09-896-095-167
4	204	44.6	59	12	US-10-038-722-112
5	204	44.6	59	12	US-09-896-095-169
6	202	44.2	58	12	US-10-167-351-69
7	201	44.0	57	12	US-10-038-722-101
8	201	44.0	57	12	US-09-896-095-158
9	201	44.0	58	12	US-10-167-351-65
10	201	44.0	61	12	US-10-038-722-109
11	201	44.0	61	12	US-09-896-095-166
12	198	43.3	57	12	US-10-038-722-100
13	198	43.3	57	12	US-09-896-095-157
14	192	42.0	58	12	US-10-167-351-75
15	192	42.0	62	12	US-10-038-722-111

16	192	42.0	62	12	US-09-896-095-168	Sequence 168, App
17	189	41.4	58	12	US-10-167-351-67	Sequence 67, App
18	189	41.4	64	12	US-10-038-722-103	Sequence 103, App
19	189	41.4	64	12	US-09-896-095-160	Sequence 160, App
20	186	40.7	58	12	US-10-167-351-71	Sequence 71, App
21	186	40.7	60	12	US-10-038-722-102	Sequence 102, App
22	186	40.7	60	12	US-09-896-095-159	Sequence 159, App
23	185	40.5	86	10	US-09-910-430-8	Sequence 8, App
24	185	40.5	86	15	US-10-165-605A-8	Sequence 8, App
25	184	40.3	58	12	US-10-038-722-55	Sequence 55, App
26	182	39.8	58	12	US-10-038-722-17	Sequence 17, App
27	182	39.8	58	12	US-10-038-722-41	Sequence 41, App
28	182	39.8	58	12	US-10-038-722-104	Sequence 104, App
29	182	39.8	58	12	US-09-896-095-161	Sequence 161, App
30	181	39.6	57	12	US-10-038-722-105	Sequence 105, App
31	181	39.6	57	12	US-09-896-095-162	Sequence 162, App
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33	181	39.6	58	12	US-10-038-722-19	Sequence 19, App
34	180	39.4	58	12	US-10-038-722-43	Sequence 43, App
35	180	39.4	58	12	US-10-038-722-49	Sequence 49, App
36	180	39.4	240	12	US-09-974-026-47	Sequence 47, App
37	180	39.4	252	9	US-09-827-948-2	Sequence 2, App
38	180	39.4	252	12	US-10-176-071-2	Sequence 2, App
39	180	39.4	252	12	US-09-974-026-49	Sequence 49, App
40	180	39.4	252	15	US-10-097-340-302	Sequence 302, App
41	180	39.4	270	12	US-10-264-049-3083	Sequence 3083, App
42	180	39.4	289	9	US-09-925-301-1266	Sequence 1266, App
43	179	39.2	58	12	US-10-167-351-62	Sequence 62, App
44	179	39.2	59	12	US-10-038-722-108	Sequence 108, App
45	179	39.2	59	12	US-09-896-095-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-038-722-5
Sequence 5, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/649,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5
Query Match 48.4%; Score 221; DB 12; Length 58;
Best Local Similarity 69.1%; Pred. No. 3.5e-18;
Matches 38; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
QY 27 RDPCFELPDTGRCVRVPPSYFYNPDKKCLBEIYGGCBGNANFTKEBCESTC 81
DB 1 RDPCFLPABTGPCRAMIRPFYNNAKSGKCEPIYGGCBGNANFTKEBCESTC 55

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RESULT 2
US-10-038-722-110
; Sequence 110, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-10-038-722-110

Query Match          46.8%; Score 214; DB 12; Length 62;
Best Local Similarity 62.7%; Pred. No. 2,4e-17;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy      25 KDRPDPCELPADGRCVRRPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCA 83
Db      1 RDRPKFCYLPADGRCCLAYMRFRYYNPASNKCKEFTIYGGCGGNANNFITMDECHTCA 59

RESULT 3
US-09-896-095-167
; Sequence 167, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 06/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-896-095-167

Query Match          46.8%; Score 214; DB 12; Length 62;
Best Local Similarity 62.7%; Pred. No. 2,4e-17;
```

```
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy      25 KDRPDPCELPADGRCVRRPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTCA 83
Db      1 RDRPKFCYLPADGRCCLAYMRFRYYNPASNKCKEFTIYGGCGGNANNFITMDECHTCA 59

RESULT 4
US-10-038-722-112
; Sequence 112, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Anemomia eulcata
US-10-038-722-112

Query Match          44.6%; Score 204; DB 12; Length 59;
Best Local Similarity 66.7%; Pred. No. 3,3e-16;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy      31 CELPDPGRCVRRPSPFYNNPDEKCKLEFIYGGCGGNANNFITKECESTC 81
Db      5 CELPKYVPCRRARPRFYNNSSKRCCKEFTIYGGCGGNANNFITLSECKVC 55

RESULT 5
US-09-896-095-169
; Sequence 169, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 06/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169
; LENGTH: 59
; TYPE: PRT
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ORGANISM: Anemonia sulcata
US-09-896-095-169

Query Match 44.6%; Score 204; DB 12; Length 59;
Best Local Similarity 66.7%; Pred. No. 3.3e-16;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 31 CELPADTGPCRVPRPSFYNNPDEKCLBFIYGGCEGNANFTKECESTC 81
DB 5 CELPKVGCGRARFPFYNNSSSKCKEKFYGGCGGNANFTKECEKVC 55

RESULT 6
US-10-167-351-69

Sequence 69, Application US/10167351
Publication No. US20030165896A1

GENERAL INFORMATION:

APPLICANT: DYAX CORP.

APPLICANT: Markland, William

APPLICANT: Ladhner, Robert C.

TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains

FILE REFERENCE: DYX-007.2P US-4

CURRENT FILING DATE: 2002-06-11

PRIOR APPLICATION NUMBER: 09/638,770

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 09/414,878

PRIOR FILING DATE: 1999-10-08

PRIOR APPLICATION NUMBER: 09/240,136

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 08/676,124

PRIOR FILING DATE: 1997-01-07

PRIOR APPLICATION NUMBER: PCT/US95/00298

PRIOR FILING DATE: 1995-01-11

PRIOR APPLICATION NUMBER: 08/208,265

PRIOR FILING DATE: 1994-03-10

PRIOR APPLICATION NUMBER: 08/179,658

PRIOR FILING DATE: 1994-01-11

NUMBER OF SEQ ID NOS: 137

SOFTWARE: Patentin version 3.1

SEQ ID NO 69

LENGTH: 58

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: designed plasmin inhibitor

US-10-167-351-69

Query Match 44.2%; Score 202; DB 12; Length 58;
Best Local Similarity 59.3%; Pred. No. 5.5e-16;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 29 DPCELPADTGPCRVPRPSFYNNPDEKCLBFIYGGCEGNANFTKECESTCA 82
DB 3 DICKLPKDTGRCARARFDKMYIDBNTKSCSEFYVGGCGGNENKKSQKCEKVC 56

RESULT 7
US-10-038-722-101

Sequence 101, Application US/10038722

Publication No. US20030175919A1

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: LADNER, Robert C.

TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS

FILE REFERENCE: LEY-1B

CURRENT APPLICATION NUMBER: US/10/038,722

CURRENT FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 08/849,406

PRIOR FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: PCT/US95/16349

PRIOR FILING DATE: 1995-12-15

PRIOR APPLICATION NUMBER: US 08/358,160

PRIOR FILING DATE: 1994-12-16

NUMBER OF SEQ ID NOS: 129

SOFTWARE: Patentin version 3.1

SEQ ID NO 101

LENGTH: 57

TYPE: PRT

ORGANISM: Naia nivea

US-10-038-722-101

Query Match 44.0%; Score 201; DB 12; Length 57;
Best Local Similarity 63.6%; Pred. No. 7.1e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 27 RDPCELPADTGPCRVPRPSFYNNPDEKCLBFIYGGCEGNANFTKECESTC 81
DB 1 RRFCELPATGTGCKARIRSFHYNRAAOCLBFIYGGCGGNANRFTIDECRTC 55

RESULT 8
US-09-896-095-158

Sequence 158, Application US/09896095

Publication No. US20030219886A1

GENERAL INFORMATION:

APPLICANT: LADNER, Charles C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: MARKLAND, William

APPLICANT: LEY, Arthur C.

APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS

FILE REFERENCE: LADNER-7L

CURRENT APPLICATION NUMBER: US/09/896,095

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 08/415,922

PRIOR FILING DATE: 1995-03-04

PRIOR APPLICATION NUMBER: 08/009,319

PRIOR FILING DATE: 1993-01-26

PRIOR APPLICATION NUMBER: 07/664,989

PRIOR FILING DATE: 1991-03-01

PRIOR APPLICATION NUMBER: 08/393,776

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 274

SOFTWARE: Patentin version 3.2

SEQ ID NO 158

LENGTH: 57

TYPE: PRT

ORGANISM: Naia nivea

US-09-896-095-158

Query Match 44.0%; Score 201; DB 12; Length 57;
Best Local Similarity 63.6%; Pred. No. 7.1e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 27 RDPCELPADTGPCRVPRPSFYNNPDEKCLBFIYGGCEGNANFTKECESTC 81
DB 1 RRFCELPATGTGCKARIRSFHYNRAAOCLBFIYGGCGGNANRFTIDECRTC 55

RESULT 9
US-10-167-351-65

Sequence 65, Application US/10167351

Publication No. US20030165896A1

GENERAL INFORMATION:

APPLICANT: DYAX CORP.

APPLICANT: Markland, William

APPLICANT: Ladhner, Robert C.

TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains

FILE REFERENCE: DYX-007.2P US-4

CURRENT APPLICATION NUMBER: US/10/167,351

;; CURRENT FILING DATE: 2002-06-11
;; PRIOR APPLICATION NUMBER: 09/638,770
;; PRIOR FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: 09/414,878
;; PRIOR FILING DATE: 1999-10-08
;; PRIOR APPLICATION NUMBER: 09/240,136
;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: 08/676,124
;; PRIOR FILING DATE: 1997-01-07
;; PRIOR APPLICATION NUMBER: PCT/US95/00298
;; PRIOR FILING DATE: 1995-01-11
;; PRIOR APPLICATION NUMBER: 08/208,265
;; PRIOR FILING DATE: 1994-03-10
;; PRIOR APPLICATION NUMBER: 08/179,658
;; PRIOR FILING DATE: 1994-01-11
;; NUMBER OF SEQ ID NOS: 137
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 65
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: designed plasmin inhibitor
US-10-167-351-65

Query Match 44.0%; Score 201; DB 12; Length 58;
Best Local Similarity 61.8%; Pred. No. 7.2e-16;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 27 RPDPCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTC 81
Db 1 ZDHPKFCYLPADGPCRKAHIFRFYIDSASNKCNKFTIYGCCEGNANFTTDECRCTCA 55

RESULT 10
US-10-038-722-109
;; Sequence 109, Application US/10038722
;; Publication No. US20030175919A1
;; GENERAL INFORMATION:
;; APPLICANT: LEY, Arthur C.
;; APPLICANT: GUTERMAN, Sonia K.
;; APPLICANT: MARKLAND, William
;; APPLICANT: KENT, Rachel B.
;; APPLICANT: ROBERTS, Bruce L.
;; APPLICANT: LADNER, Robert C.
;; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
;; FILE REFERENCE: LEY-1B
;; CURRENT APPLICATION NUMBER: US/10/038,722
;; CURRENT FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 08/849,406
;; PRIOR FILING DATE: 1999-07-21
;; PRIOR APPLICATION NUMBER: PCT/US95/16349
;; PRIOR FILING DATE: 1995-12-15
;; PRIOR APPLICATION NUMBER: US 08/358,160
;; PRIOR FILING DATE: 1994-12-16
;; NUMBER OF SEQ ID NOS: 129
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 109
;; LENGTH: 61
;; TYPE: PRT
;; ORGANISM: Vipera ammodytes
US-10-038-722-109

Query Match 44.0%; Score 201; DB 12; Length 61;
Best Local Similarity 57.6%; Pred. No. 7.6e-16;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 25 KDRPDCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTCA 83
Db 1 ZDHPKFCYLPADGPCRKAHIFRFYIDSASNKCNKFTIYGCCEGNANFTTDECRCTCA 59

RESULT 11

US-09-896-095-166
;; Sequence 166, Application US/09896095
;; Publication No. US20030219866A1
;; GENERAL INFORMATION:
;; APPLICANT: LADNER, Charles C.
;; APPLICANT: GUTERMAN, Sonia K.
;; APPLICANT: ROBERTS, Bruce L.
;; APPLICANT: MARKLAND, William
;; APPLICANT: LEY, Arthur C.
;; APPLICANT: KENT, Rachel B.
;; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
;; FILE REFERENCE: LADNER-71
;; CURRENT APPLICATION NUMBER: US/09/896,095
;; CURRENT FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: 08/415,922
;; PRIOR FILING DATE: 1995-03-04
;; PRIOR APPLICATION NUMBER: 08/009,319
;; PRIOR FILING DATE: 1993-01-26
;; PRIOR APPLICATION NUMBER: 07/664,989
;; PRIOR FILING DATE: 1991-03-01
;; PRIOR APPLICATION NUMBER: 08/993,776
;; PRIOR FILING DATE: 1997-12-18
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO: 166
;; LENGTH: 61
;; TYPE: PRT
;; ORGANISM: Vipera ammodytes
US-09-896-095-166

Query Match 44.0%; Score 201; DB 12; Length 61;
Best Local Similarity 57.6%; Pred. No. 7.6e-16;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 25 KDRPDCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTCA 83
Db 1 ZDHPKFCYLPADGPCRKAHIFRFYIDSASNKCNKFTIYGCCEGNANFTTDECRCTCA 59

RESULT 12
US-10-038-722-100
;; Sequence 100, Application US/10038722
;; Publication No. US20030175919A1
;; GENERAL INFORMATION:
;; APPLICANT: LEY, Arthur C.
;; APPLICANT: GUTERMAN, Sonia K.
;; APPLICANT: MARKLAND, William
;; APPLICANT: KENT, Rachel B.
;; APPLICANT: ROBERTS, Bruce L.
;; APPLICANT: LADNER, Robert C.
;; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
;; FILE REFERENCE: LEY-1B
;; CURRENT APPLICATION NUMBER: US/10/038,722
;; CURRENT FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 08/849,406
;; PRIOR FILING DATE: 1999-07-21
;; PRIOR APPLICATION NUMBER: PCT/US95/16349
;; PRIOR FILING DATE: 1995-12-15
;; PRIOR APPLICATION NUMBER: US 08/358,160
;; PRIOR FILING DATE: 1994-12-16
;; NUMBER OF SEQ ID NOS: 129
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 100
;; LENGTH: 57
;; TYPE: PRT
;; ORGANISM: Hemachatus hemachatus
US-10-038-722-100

Query Match 43.3%; Score 198; DB 12; Length 57;
Best Local Similarity 61.8%; Pred. No. 1.6e-15;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 27 RPDPCFLPADTGPCRVAPSPFYNNPDEKCKLEFIYGCCEGNANFTTKECESTC 81

Db 1 RDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 55

RESULT 13
US-09-896-095-157

Sequence 157, Application US/09896095
Publication No. US20030219886A1
GENERAL INFORMATION:
APPLICANT: LADNER, Charles C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: LEY, Arthur C.
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
FILE REFERENCE: LADNER-7L
CURRENT APPLICATION NUMBER: US/09/896,095
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 08/415,922
PRIOR FILING DATE: 1995-03-04
PRIOR APPLICATION NUMBER: 08/009,319
PRIOR FILING DATE: 1993-01-26
PRIOR APPLICATION NUMBER: 07/664,989
PRIOR FILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 08/993,776
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn version 3.2
SEQ ID NO 157
LENGTH: 57
TYPE: PRT
ORGANISM: Hemachatus hemachatus
US-09-896-095-157

Query Match 43.3%; Score 198; DB 12; Length 57;
Best Local Similarity 61.8%; Pred. No. 1.6e-15;
Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 27 RDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 81
Db 1 RDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 55

RESULT 14
US-10-167-351-75

Sequence 75, Application US/10167351
Publication No. US20030165896A1
GENERAL INFORMATION:
APPLICANT: DYAX CORP.
APPLICANT: Markland, William
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
FILE REFERENCE: DYX-007.2P US-4
CURRENT APPLICATION NUMBER: US/10/167,351
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 09/638,770
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 09/414,878
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/240,136
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 08/676,124
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: PCT/US95/00298
PRIOR FILING DATE: 1995-01-11
PRIOR APPLICATION NUMBER: 08/208,265
PRIOR FILING DATE: 1994-03-10
PRIOR APPLICATION NUMBER: 08/179,658
PRIOR FILING DATE: 1994-01-11
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75

LENGTH: 58
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: designed plasmin inhibitor
US-10-167-351-75

Query Match 42.0%; Score 192; DB 12; Length 58;
Best Local Similarity 54.5%; Pred. No. 7.9e-15;
Matches 30; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 28 PDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 82
Db 2 PDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 56

RESULT 15
US-10-038-722-111

Sequence 111, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITT-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 111
LENGTH: 62
TYPE: PRT
ORGANISM: Bungarus fasciatus
US-10-038-722-111

Query Match 42.0%; Score 192; DB 12; Length 62;
Best Local Similarity 57.6%; Pred. No. 8.5e-15;
Matches 34; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 83
Db 1 KDPFCELPAETGCKAYIRSFHYNLAQOCTLPYGGCGGNANRFTIDECCRTCC 59

Search completed: January 23, 2004, 10:43:29
Job time : 29.8099 sec

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OM protein - protein search, using SW model

Run on: January 23, 2004, 10:22:13 (Search time 13.7359 Seconds
(without alignments)
255.666 Million cell updates/sec)

Title: US-09-700-179A-16

Sequence: 1 MSGGILLILGLTWELT.....CEGNANFTKESSTCA 83

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Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgm2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgm2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgm2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	221	48.4	58	1	US-08-358-160-71
2	217	47.5	65	6	5466783-12
3	214	46.8	65	1	US-08-358-160-92
4	204	44.6	62	1	US-08-358-160-97
5	202	44.2	58	3	US-08-676-124-69
6	202	44.2	58	3	US-09-414-878-69
7	202	44.2	58	3	US-09-240-136-69
8	202	44.2	58	4	US-09-638-770A-69
9	201	44.0	57	1	US-08-358-160-99
10	201	44.0	58	3	US-08-676-124-65
11	201	44.0	58	3	US-09-414-878-65
12	201	44.0	58	3	US-09-240-136-65
13	201	44.0	58	4	US-09-638-770A-65
14	201	44.0	61	1	US-08-358-160-91
15	198	43.3	57	1	US-08-358-160-94
16	198	43.3	57	6	5466783-9
17	195	42.7	61	1	US-08-358-160-93
18	194	42.5	57	1	US-08-358-160-108
19	192.5	42.1	60	6	5466783-8
20	192	42.0	58	3	US-08-676-124-75
21	192	42.0	58	3	US-09-414-878-75
22	192	42.0	58	3	US-09-240-136-75
23	192	42.0	58	4	US-09-638-770A-75
24	192	42.0	65	1	US-08-358-160-96
25	190.5	41.7	58	6	5466783-10
26	189	41.4	58	3	US-08-676-124-67
27	189	41.4	58	3	US-09-414-878-67

28	189	41.4	58	3	US-09-240-136-67	Sequence 67, Appl
29	189	41.4	58	4	US-09-638-770A-67	Sequence 67, Appl
30	189	41.4	66	1	US-08-358-160-113	Sequence 113, App
31	189	41.4	79	6	5466783-7	Patent No. 5466783
32	188	41.1	58	1	US-08-358-160-116	Sequence 116, App
33	186	40.7	58	3	US-08-676-124-71	Sequence 71, Appl
34	186	40.7	58	3	US-09-414-878-71	Sequence 71, Appl
35	186	40.7	58	3	US-09-240-136-71	Sequence 71, Appl
36	186	40.7	58	4	US-09-638-770A-71	Sequence 71, Appl
37	186	40.7	60	1	US-08-358-160-95	Sequence 95, Appl
38	181	39.6	57	1	US-08-358-160-103	Sequence 103, App
39	181	39.6	58	1	US-08-358-160-17	Sequence 17, Appl
40	181	39.6	58	1	US-08-358-160-18	Sequence 18, Appl
41	180	39.4	58	1	US-08-358-160-12	Sequence 12, Appl
42	180	39.4	240	4	US-09-144-428-47	Sequence 47, Appl
43	180	39.4	252	1	US-08-685-660A-7	Sequence 7, Appl
44	180	39.4	252	2	US-08-974-195-7	Sequence 7, Appl
45	180	39.4	252	3	US-09-071-709-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-358-160-71
Sequence 71, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION/DOCKET NUMBER: 28, 005
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-71

Query Match 48.4%; Score 221; DB 1; Length 58;
Best Local Similarity 69.1%; Pred. No. 3.1e-20;
Matches 38; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 27 RPDCELPAADTGCRVRFPSPFYNNPDEKCLEFIYGGCGGNANNFTKEBCSTC 81
Db 1 RDPFCFLPADTGCRVAMTPRYNNKSGKCEPFYGGCGGNANNFTKEBCRTC 55

RESULT 2
5466783-12
Patent No. 5466783
APPLICANT: Wun, Tze-Chen, Kretzmer, Kuniko K., Broze,
George J. Jr.
TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
NUMBER OF SEQUENCES: 26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/93,285
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,280
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 123,753
FILING DATE: 23-NOV-1987
APPLICATION NUMBER: 77,366
FILING DATE: 23-JUL-1987
SEQ ID NO: 12
LENGTH: 65
5466783-12

Query Match 47.5%; Score 217; DB 6; Length 65;
Best Local Similarity 62.7%; Pred. No. 1.1e-19;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPFCFLPADTGCRVRFPSPFYNNPDEKCLEFIYGGCGGNANNFTKEBCSTCA 83
Db 1 RDRPFCTLPADPGRCLAYMPRFYNNPASNCKEFTYGGCGGNANNFTKWDECRHTCVA 59

RESULT 3
US-08-358-160-92
Sequence 92, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-92

Query Match 46.8%; Score 214; DB 1; Length 65;
Best Local Similarity 62.7%; Pred. No. 2.6e-19;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 25 KDRPFCFLPADTGCRVRFPSPFYNNPDEKCLEFIYGGCGGNANNFTKEBCSTCA 83
Db 1 RDRPFCTLPADPGRCLAYMPRFYNNPASNCKEFTYGGCGGNANNFTKWDECRHTCVA 59

RESULT 4
US-08-358-160-97
Sequence 97, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-97

Query Match 44.6%; Score 204; DB 1; Length 62;
Best Local Similarity 66.7%; Pred. No. 4.2e-18;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Cy 31 CELPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANPITKECESTC 81
Db 5 CELPKVGPGRARFPRTYNNSSKRCCKFYGGCGGNANPHTLECEKVC 55

RESULT 5
US-08-676-124-69
Sequence 69, Application US/08676124
Patent No. 6010880
GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSER: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND=3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-69

Query Match 44.2%; Score 202; DB 3; Length 58;
Best Local Similarity 59.3%; Pred. No. 6.8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Cy 29 DFCLEPADTGPCRVPRPSFYNNPDEKCKLEFYGGCGGNANPITKECESTCA 82
Db 3 DICKLPDTPGCRARFPDKWYDNTKSCSEFYGGCGGNANPKFSQKECEKVC 56

RESULT 6
US-09-414-878-69
Sequence 69, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSER: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-69

Query Match 44.2%; Score 202; DB 3; Length 58;
Best Local Similarity 59.3%; Pred. No. 6,8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 29 DCELPADTGPGRVRFPSFYNNPDEKCKLEFYGGCGGNANPITKECESTCA 82
Db 3 DICKLPKDTGCRARFDMKYDDPNTKSCERFYGGCGGNENKFGSQKECEKCA 56

RESULT 7
US-09-240-136-69
Sequence 69, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kuntz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSER: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P

REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-69

Query Match 44.2%; Score 202; DB 3; Length 58;
Best Local Similarity 59.3%; Pred. No. 6,8e-18;
Matches 32; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 29 DCELPADTGPGRVRFPSFYNNPDEKCKLEFYGGCGGNANPITKECESTCA 82
Db 3 DICKLPKDTGCRARFDMKYDDPNTKSCERFYGGCGGNENKFGSQKECEKCA 56

RESULT 8
US-09-638-770A-69
Sequence 69, Application US/09638770A
Patent No. 6423498
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kuntz Domains
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSER: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,770A
FILING DATE: 15-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-638-770A-69

Query Match	44.2%	Score 202;	DB 4;	Length 58;
Best Local Similarity	59.3%	Pred. No. 6.8e-18;		
Matches 32; Conservative	8;	Mismatches 14;	Indels 0;	Gaps 0;

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Qy 29 DFCGLPADTGGPCVRFPSPFYNNPDEKKCLBFIYGGCEBGNANPITKEEESTCA 82
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 3 DIKLPKDTGPCRARFDKWTYDPTKSCSEFVGGCGGNNKFGSQKECEKVCVA 56

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```

1      RESULT 9
2      US-08-358-160-99
3      Sequence 99, Application US/08358160
4      Patent No. 5663143
5      GENERAL INFORMATION:
6      APPLICANT: LEV, Arthur C.
7      APPLICANT: LADNER, Robert C.
8      APPLICANT: GUTERMAN, Sonia K.
9      APPLICANT: ROBERTS, Bruce L.
10     APPLICANT: MARKLAND, William
11     APPLICANT: KENT, Rachel B.
12     TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
13     TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
14     NUMBER OF SEQUENCES: 234
15     CORRESPONDENCE ADDRESS:
16     ADDRESSEE: BROWDY AND NETWORK
17     STREET: 419 Seventh Street, N.W. Suite 300
18     CITY: Washington
19     STATE: District of Columbia
20     COUNTRY: USA
21     ZIP: 20004
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS
26     SOFTWARE: PatentIn Release #1.0, Version #1.25
27     CURRENT APPLICATION DATA:
28     APPLICATION NUMBER: US/08/358,160
29     FILING DATE: 16-DEC-1994
30     CLASSIFICATION: 514
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: US 08/133,031
33     FILING DATE: 13-OCT-1993
34     PRIOR APPLICATION DATA:
35     APPLICATION NUMBER: US 08/009,319
36     FILING DATE: 26-JAN-1993
37     PRIOR APPLICATION DATA:
38     APPLICATION NUMBER: US 07/664,989
39     FILING DATE: 01-MAR-1991
40     PRIOR APPLICATION DATA:
41     APPLICATION NUMBER: US 07/487,063
42     FILING DATE: 02-MAR-1990
43     PRIOR APPLICATION DATA:
44     APPLICATION NUMBER: US 07/240,160
45     FILING DATE: 02-SEP-1988
46     ATTORNEY/AGENT INFORMATION:
47     NAME: Cooper, Iver P.
48     REGISTRATION NUMBER: 28,005
49     REFERENCE/DOCKET NUMBER: LEY-1
50     TELECOMMUNICATION INFORMATION:
51     TELEPHONE: 202-628-5197
52     TELEFAX: 202-737-3528
53     TELEX: 248633
54     INFORMATION FOR SEQ ID NO: 99:
55     SEQUENCE CHARACTERISTICS:
56     LENGTH: 57 amino acids
57     TYPE: amino acid
58     STRANDEDNESS: single
59     TOPOLOGY: linear
60     MOLECULE TYPE: protein
61     US-08-358-160-99

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Query Match          44.0%; Score 201; DB 1; Length 57;
Best Local Similarity 63.6%; Pred. No. 8,9e-18;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Cy 27 RPDCELPADTGPCKRVPPSPFYNNPDEKCLEFIYGCCEGNANNFITKECESTC 81
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1 RPRCELPARTGCLKARIRSFHYVRAAOCCLEFIYGCCEGNANNFITIDECHRTC 55

RESULT 10
US-08-676-124-65
; Sequence 65, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Broadway and Nelmark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND=3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-676-124-65

Query Match          44.0%; Score 201; DB 3; Length 58;
Best Local Similarity 61.8%; Pred. No. 9.1e-18;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Cy 27 RPDCELPADTGPCKRVPPSPFYNNPDEKCLEFIYGCCEGNANNFITKECESTC 81
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1 KPDECFLBEDYGPCRGFRDRFYNNQTKQCTFIYGCCEGNANNFETLEBCKNIC 55

RESULT 11
US-09-414-878-65
; Sequence 65, Application US/09414878

```

RESULT 11
US-09-414-878-65
; Sequence 65, Application US/09414878

CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,770A
FILING DATE: 15-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ZWICKER, Kenneth P.
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-638-770A-65

Query Match 44.0%; Score 201; DB 4; Length 58;
Best Local Similarity 61.8%; Pred. No. 9.1e-18;
Matches 34; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 27 RPPDFCELPADTGPCVRPSPFYNNPDEKCKLEFYGGCGGNANNFITKECESTC 81
DB 1 KPDPFCELPDTPGCRGAFDRIFNNQKCTFIYGGCGGNANNFETIECKNIC 55

RESULT 14
US-08-358-160-91
Sequence 91, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iyer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-91

Query Match 44.0%; Score 201; DB 1; Length 61;
Best Local Similarity 57.6%; Pred. No. 9.6e-18;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 25 KDPDFCELPADTGPCVRPSPFYNNPDEKCKLEFYGGCGGNANNFITKECESTCA 83
DB 1 QDPKFCYLPADPGRCAHIFRFFYDSASNNKKNFYGGCGGNANNFITWECROTCA 59

RESULT 15
US-08-358-160-94
Sequence 94, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160
 FILING DATE: 16-DEC-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/133,031
 FILING DATE: 13-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,319
 FILING DATE: 26-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/664,989
 FILING DATE: 01-MAR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/487,063
 FILING DATE: 02-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/240,160
 FILING DATE: 02-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Cooper, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: 187-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-358-160-94

Query Match: 43.3%; Score 198; DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 2,1e-17;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 27 RPDPELADNTPGCVRPSPFYNPDEKKCLEFTYGGCGGNANFTYKECESTC 81
 Db 1 RPDPELPAETGLCKAYIRSFHYNLAQOCLQFIYGGCGGNANRFTIDECHRTC 55

Search completed: January 23, 2004, 10:29:11
 Job time : 13.7359 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 40.0387 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179a-16

Sequence: 1 MSKGLLLGLLTWEVL.....CEGNANPIKESCESTCAA 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	457	100.0	83	21	AAV15145
2	438	95.8	83	21	AAV15146
3	361	79.0	83	21	AAV15147
4	343	75.1	83	21	AAV15150
5	342	74.8	83	21	AAV15149
6	341	74.6	59	21	AAV15138
7	334	73.1	60	21	AAV15148
8	334	73.1	60	21	AAV15153
9	322	70.5	59	21	AAV15139

10	299	65.4	60	21	AAV15151
11	298	65.2	60	21	AAV15154
12	245	53.6	59	21	AAV15140
13	227	49.7	59	21	AAV15143
14	226	49.5	59	21	AAV15142
15	225	49.2	59	21	AAV15141
16	221	48.4	58	17	AAV15146
17	201	44.0	58	16	AAV178542
18	196	42.9	58	16	AAV178546
19	192	42.0	58	16	AAV178552
20	189	41.4	58	16	AAV178544
21	185.5	40.6	145	18	AAV25935
22	185.5	40.6	165	18	AAV25937
23	185	40.5	86	22	AAV25938
24	185	40.5	124	18	AAV25933
25	185	40.5	144	18	AAV25938
26	184	40.5	58	17	AAV19197
27	183	40.0	55	18	AAV25931
28	183	40.0	124	18	AAV25932
29	183	40.0	144	18	AAV25936
30	182	39.8	58	17	AAV19158
31	182	39.8	58	17	AAV19182
32	181	39.6	58	13	AAV27492
33	181	39.6	58	17	AAV19159
34	181	39.6	58	17	AAV19160
35	181	39.6	252	22	AAV25926
36	180	39.4	58	13	AAV27396
37	180	39.4	58	17	AAV19191
38	180	39.4	58	17	AAV19184
39	180	39.4	240	21	AAV30045
40	180	39.4	240	21	AAV14185
41	180	39.4	252	18	AAV30040
42	180	39.4	252	18	AAV13665
43	180	39.4	252	19	AAV70286
44	180	39.4	252	21	AAV17719
45	180	39.4	252	21	AAV14187

ALIGNMENTS

RESULT 1	AAV15145	standard; Protein; 83 AA.
XX	AAV15145	
AC	AAV15145;	
XX		
DT	07-FEB-2000 (first entry)	
XX		
DE	Proform of Txln 1 protein.	
XX		
KW	Textilinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;	
KW	Australian brown snake; conserved cysteine residue; stability; Apricotin;	
KW	haematopoietic; cytosolic activity; homology; specificity; control;	
KW	Tatocroxin-associated plasmin inhibitor; TAC; inhibitory efficiency;	
KW	fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;	
KW	fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;	
KW	reduced propensity; chromosome.	
XX		
OS	Pseudonaja textilis textilis.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..24
FT	Protein	/label= Leader_peptide
FT		25..83
FT		/label= Txln-1 protein
XX		/note= "Textilinin-1"
XX	W09958569-A1.	
XX		
PD	18-NOV-1999.	
XX		
PF	07-MAY-1999;	.99WO-AU00343.

Plasmin Inhibitor
Plasmin Inhibitor
Txln 3 plasmin inh
Txln 6 plasmin inh
Txln 5 plasmin inh
Txln 4 plasmin inh
Apricotin-like Kun
Human LACI-K2 dext
Human collagen alp
Human TPEI-2 domai
Human LACI-K3 deri
Novel protease inh
Elastase inhibitor
I. ricinus salivar
New protease inhib
SUC2-Ep7-d21-RPDI
Genetically engine
RPDI-Kunitz domain
New protease inhib
SUC2-Ep1-d21-RPDI
Genetically engine
Genetically engine
Human neutrophil e
Genetically engine
Kunitz type 2 Ser
Human neutrophil e
Genetically engine
Human placental bi
Human placental bi
Hepatocyte growth
Human tissue facto
Human kunitz type
Human placental bi

XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV,
 XX WPI; 2000-039073/03.
 DR N-PSDB; AA229024.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX Claim 40a; Page 71; 112pp; English.
 XX The present sequence is the proform of the Textillinin protein, Txln 1,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 45st and
 CC 58th homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 XX Sequence 83 AA;
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 Query Match 100.0%; Score 457; DB 21; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSGGLLLLLGLTTWEVLTPIVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPT 60
 DB 1 MSSGGLLLLLGLTTWEVLTPIVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPT 60
 QY 61 YGGCGNNANPITKECESTCA 83
 DB 61 YGGCGNNANPITKECESTCA 83
 RESULT 2
 AAY15146
 ID AAY15146 standard; Protein; 83 AA.
 AC AAY15146;
 DT 07-FEB-2000 (first entry)
 XX Proform of Txln 2 protein.
 DE
 XX Textillinin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KW haematopoietic; cytostatic activity; homology; specificity; control;
 KW Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX Key Location/Qualifiers
 PH 1..24
 FT /label= leader_peptide
 FT 25..83
 FT Protein
 FT /label= Txln-2_protein

FT /note= "Textillinin-2"
 XX MO9958569-A1.
 XX 18-NOV-1999.
 PD 07-MAY-1999; 99MO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAF/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV,
 XX WPI; 2000-039073/03.
 DR N-PSDB; AA229025.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX Claim 40b; Page 71; 112pp; English.
 XX The present sequence is the proform of the Textillinin protein, Txln 2,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 2 has 43th and
 CC 55th homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 XX Sequence 83 AA;
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 Query Match 95.8%; Score 438; DB 21; Length 83;
 Best Local Similarity 95.2%; Pred. No. 2.2e-44;
 Matches 79; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MSSGGLLLLLGLTTWEVLTPIVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPT 60
 DB 1 MSSGGLLLLLGLTTWEVLTPIVSSKDRPDCPLPDTGRCRVRFPSFYNNPDKCLEPT 60
 QY 61 YGGCGNNANPITKECESTCA 83
 DB 61 YGGCGNNANPITKECESTCA 83
 RESULT 3
 AAY15147
 ID AAY15147 standard; Protein; 83 AA.
 AC AAY15147;
 DT 07-FEB-2000 (first entry)
 XX Proform of Txln 3 protein.
 DE
 XX Textillinin proform; Txln 3; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.

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XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-3 protein
FT /note= "Textilinin-3"
XX
XX MO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M P.
XX (GAFV/) GAFNEY P J.
XX
XX Maaci PP, Lavin MF, Gafney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX N-PSDB; AAZ29026.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40c; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 3,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 83 AA.
XX
XX Query Match 79.0%; Score 361; DB 21; Length 83;
XX Best Local Similarity 77.1%; Pred. No. 3.2e-35;
XX Matches 64; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
XX
XX QY 1 MSSGGLLLGLLTMEVLTTPVSSKDRPFCGLPADTGCRVRFPSPFYNPBEKKLEFI 60
XX DB 1 MSSGGLLLGLLTMEVLTTPVSSKDRPFCGLPADTGCRVRFPSPFYNPBEKKLEFI 60
XX
XX QY 61 YGCGGNANNPFTKECESTCA 83
XX DB 61 YGCGGNANNPFTKECESTCA 83
XX
XX RESULT 4
XX ID AAY15150 standard; Protein; 83 AA.
XX AC AAY15150;
XX DT 07-FEB-2000 (first entry)
XX DE Proform of Txln 6 protein.
XX
XX Textilinin proform; Txln 6; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;

```

```

XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Leader_peptide
FT Protein 25..83
FT /label= Txln-6 protein
FT /note= "Textilinin-6"
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XX MO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M P.
XX (GAFV/) GAFNEY P J.
XX
XX Maaci PP, Lavin MF, Gafney PJ, Sorokina NI, Filipovich IV;
XX WPI; 2000-039073/03.
XX N-PSDB; AAZ29029.
XX
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40f; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textilinin protein, Txln 6,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 83 AA.
XX
XX Query Match 75.1%; Score 343; DB 21; Length 83;
XX Best Local Similarity 77.1%; Pred. No. 4.5e-33;
XX Matches 64; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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XX QY 1 MSSGGLLLGLLTMEVLTTPVSSKDRPFCGLPADTGCRVRFPSPFYNPBEKKLEFI 60
XX DB 1 MSSGGLLLGLLTMEVLTTPVSSKDRPFCGLPADTGCRVRFPSPFYNPBEKKLEFI 60
XX
XX QY 61 YGCGGNANNPFTKECESTCA 83
XX DB 61 YGCGGNANNPFTKECESTCA 83
XX
XX RESULT 5
XX ID AAY15149 standard; Protein; 83 AA.
XX AC AAY15149;
XX DT 07-FEB-2000 (first entry)
XX

```

DE Perform of Txln 5 protein.

XX Textillin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

OS

XX Key Location/Qualifiers
 FH 1..24
 FT /label= Leader_peptide
 FT 25..83
 FT Protein /label= Txln-5 Protein
 FT /note= "Textillin-5"

XX WO9958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAFV/) GAFNEY P J.

XX Mascl PP, Layin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 WPI: 2000-039073/03.
 DR N-PSDB; AA229028.

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -

XX Claim 40e; Page 72; 112pp; English.

XX The present sequence is the proform of the Textillin protein, Txln 5,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX Sequence 83 AA;

XX Query Match 74.8%; Score 342; DB 21; Length 83;
 XX Best Local Similarity 77.1%; Pred. No. 5..9e-33;
 XX Matches 64; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSSGGILLGLTLMENVLPVSSKDRPFCBLPADTGCRVAFPSFYNPDEKCKLEFI 60
 DB 1 MSSGGILLGLTLMENVLPVSSKDRPFCBLPADTGCRVAFPSFYNPDEKCKLEFI 60

QY 61 YGCGEGNANNFITKECESTCA 83
 DB 61 YGCGEGNANNFITKECESTCA 83

RESULT 6
 AAAY15138 standard; Protein; 59 AA.

XX AC AAY15138;
 XX 07-FEB-2000 (first entry)

XX Txln 1 Plasmin inhibitor protein.

DE

XX Textillin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; homology; specificity; Apoptin;
 KW Talocotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

OS

XX WO9958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAFV/) GAFNEY P J.

XX Mascl PP, Layin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 WPI: 2000-039073/03.
 DR N-PSDB; AA229017.

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -

XX Claim 8a; Page 68; 112pp; English.

XX The present sequence is the Textillin protein, Txln 1, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 1 has 45% and
 CC 58% homology with Apoptin and Talocotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.

XX Sequence 59 AA;

XX Query Match 74.6%; Score 341; DB 21; Length 59;
 XX Best Local Similarity 100.0%; Pred. No. 5.2e-33;
 XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 KDRPDCBLPADTGCRVAFPSFYNPDEKCKLEFIYGGCGEGNANNFITKECESTCA 83
 DB 1 KDRPDCBLPADTGCRVAFPSFYNPDEKCKLEFIYGGCGEGNANNFITKECESTCA 59

RESULT 7
 AAAY15148 standard; Protein; 83 AA.

XX AC AAY15148;
 XX 07-FEB-2000 (first entry)

XX DE Proform of Txln 4 protein.
 XX XX
 KM Textillinin proform; Txln 4; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX OS
 XX Pseudonaja textilis textilis.
 XX XX
 FH Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader_peptide
 FT Protein 25..83
 FT /label= Txln-4 protein
 FT /note= "Textillinin-4"
 FT
 XX MO9958569-A1.
 XX PN
 XX PD 18-NOV-1999.
 XX PP 07-MAY-1999; 99WO-AU00343.
 XX PR 11-MAY-1998; 98AU-0003450.
 XX XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFV/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gafney PJ, Sorokina NI, Philippovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ20927.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 40d; Page 72; 112pp; English.
 XX
 CC The present sequence is the proform of the Textillinin protein, Txln 4,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC XX
 SQ Sequence 83 AA;
 Query Match 74.6%; Score 341; DB 21; Length 83;
 Best Local Similarity 77.1%; Pred. No. 7.7e-33;
 Matches 64; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 MSSGGILLILGLITTWELTPVSSKDRPFCPLPADTGCRCRPFSPYNNPBEKCLERT 60
 DB 1 MSSGGILLILGLITTWELTPVSSKDRPFCPLPADTGCRCRPFSPYNNPBEKCLERT 60
 OY 61 YGCGGNANNTFKKECESTCAA 83
 DB 61 YGCGGNANNTFKKECESTCAA 83

ID AAY15153 standard; Protein; 60 AA.
 XX AC AAY15153;
 XX XX
 DT 07-FEB-2000 (first entry)
 XX DE Plasmin inhibitor Txln 1, encoded by partial cDNA sequence.
 XX XX
 KM Textillinin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytosolic activity; homology; specificity; enzyme;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; cDNA;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM inhibitory efficiency; reduced propensity; thrombosis.
 XX OS
 XX Pseudonaja textilis textilis.
 XX XX
 FH Key Location/Qualifiers
 FH Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 47
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"
 FT
 XX MO9958569-A1.
 XX PN
 XX PD 18-NOV-1999.
 XX PP 07-MAY-1999; 99WO-AU00343.
 XX PR 11-MAY-1998; 98AU-0003450.
 XX XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFV/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gafney PJ, Sorokina NI, Philippovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ29047.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Disclosure; Fig 6; 112pp; English.
 XX
 CC The present amino acid sequence is the Txln 1, Textillinin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for
 CC alleviating blood loss, following major surgery or trauma. Conjugates of
 CC the plasmin inhibitor and an anti-fibrin antibody are useful as
 CC anti-tumour agents. They have reduced propensity to cause thrombosis.
 CC XX
 SQ Sequence 60 AA;
 Query Match 73.1%; Score 334; DB 21; Length 60;
 Best Local Similarity 96.6%; Pred. No. 3.6e-32;
 Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 25 KDRPFCPLPADTGCRCRPFSPYNNPBEKCLERTYGGCGGNANNTFKKECESTCAA 83
 DB 2 KDRPFCPLPADTGCRCRPFSPYNNPBEKCLERTYGGCGGNANNTFKKECESTCGS 60

ID AAY15139 standard; Protein; 59 AA.
 XX
 AC AAY15139;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Txln 2 Plasmin inhibitor protein.
 XX
 KW Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytosolic activity; homology; specificity; Aprotinin;
 KW Talcotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 PI WPI, 2000-039073/03.
 DR N-PSDB; AA229018.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 8b; Page 69; 112pp; English.
 XX
 CC The present sequence is the Textillin protein, Txln 2 that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln 2 has 43% and
 CC 55% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 59 AA;
 XX
 Query Match 70.5%; Score 322; DB 21; Length 59;
 Best Local Similarity 93.2%; Pred. No. 9, 4e-11;
 Matches 55; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 25 KDRPFCRLPADTGPCRVPPSPRYNPPDEKCKLEFIYGGCEGANNFTKECESTCAA 83
 DB 1 KDRPFCRLPADTGPCRVPPSPRYNPPDEKCKLEFIYGGCEGANNFTKECESTCAA 59

RESULT 10
 ID AAY15151 standard; Protein; 60 AA.
 XX
 AC AAY15151;
 XX

DT 07-FEB-2000 (first entry)
 XX
 DE Plasmin inhibitor Txln 1, partial protein sequence.
 XX
 KW Textillin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW rapid amplification of cDNA end; RACE; reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PN MO9958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 PI WPI, 2000-039073/03.
 DR N-PSDB; AA229030.
 XX
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Example 2; Page 108; 112pp; English.
 XX
 CC The present sequence is the partial Txln 1, Textillin protein sequence.
 CC It is obtained by sequence analysis of the 5' and 3' RACE products. It is
 CC a single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln 1 has 45% and
 CC 58% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 XX
 SQ Sequence 60 AA;
 XX
 Query Match 65.4%; Score 299; DB 21; Length 60;
 Best Local Similarity 91.7%; Pred. No. 5, 3e-28;
 Matches 55; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 MSSGILLILGLITLMEVLTTPVSSKDRPFCRLPADTGPCRVPPSPRYNPPDEKCKLEFI 60
 DB 1 MSSGILLILGLITLMEVLTTPVSSKDRPFCRLPADTGPCRVPPSPRYNPPDEKCKLEFI 60

RESULT 11
 ID AAY15154 standard; Protein; 60 AA.
 XX

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XX AC AAY15154;
XX DT 07-FEB-2000 (first entry)
XX DE Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.
XX KM Textillinin protein; Txln 2, plasmin inhibitor; single stage inhibitor;
XX KM Australian brown snake; conserved cysteine residue; stability; control;
XX KM haematopoietic; cytosolic activity; homology; enzyme;
XX KM fluidity of blood; alleviate; blood loss; major surgery; trauma;
XX KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX KM inhibitory efficiency; reduced propensity; thrombosis.
XX OS Pseudonaja textilis textilis.
XX FH Key Location/Qualifiers
XX FT Misc-difference 24 /note= "encoded by TTG"
XX FT Misc-difference 45 /note= "encoded by GAT"
XX FT Misc-difference 49 /note= "encoded by ATG"
XX FT Misc-difference 59 /note= "encoded by CCN"
XX PN MO958569-A1.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99WO-AU00343.
XX PR 11-MAY-1998; 98AU-0003450.
XX PA (UYOU ) UNIV QUEENSLAND.
XX PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX PA (MASC/) MASI P P.
XX PA (LAVI/) LAVIN M F.
XX PA (GAFV/) GAFNEY P J.
XX PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX DR WPI; 2000-039073/03.
XX DR N-PSDB; AAZ29048.
XX PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX PT agents -
XX PS Disclosure; Fig 7; 112pp; English.
XX PS The present amino acid sequence is the Txln 2, Textillinin protein
XX CC encoded by the partial cDNA sequence. It is a single stage competitive
XX CC inhibitor of plasmin. It is isolated from the Australian brown snake,
XX CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
XX CC low inhibitory efficiency that can transiently affect the delicate
XX CC balance between enzymes and inhibitors of the fibrinolytic system,
XX CC controlling the fluidity of blood. The plasmin inhibitors are useful for
XX CC alleviating blood loss, following major surgery or trauma. Conjugates of
XX CC the plasmin inhibitor and an anti-fibrin antibody are useful as
XX CC anti-tumour agents. They have reduced propensity to cause thrombosis.
XX SQ Sequence 60 AA;
XX Query Match 65.2%; Score 298; DB 21; Length 60;
XX Best Local Similarity 89.5%; Pred. No. 6.9e-28;
XX Matches 51; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 25 KDRPFCLEPADTGPCRVFPSPFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 81
DB 2 KDRPFCLEPADTGPCRVFPSPFYNNPDEKCLBFIYGGCEGNANNFITKECESTC 58

RESULT 12

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AAY15140
ID AAY15140 standard; Protein; 59 AA.
XX AC AAY15140;
XX DT 07-FEB-2000 (first entry)
XX DE Txln 3 Plasmin inhibitor protein.
XX KM Textillinin protein; Txln 3, plasmin inhibitor; single stage inhibitor;
XX KM Australian brown snake; conserved cysteine residue; stability; control;
XX KM haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
XX KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX KM reduced propensity; thrombosis.
XX OS Pseudonaja textilis textilis.
XX FH Key Location/Qualifiers
XX FT Misc-difference 24 /note= "encoded by TTG"
XX FT Misc-difference 45 /note= "encoded by GAT"
XX FT Misc-difference 49 /note= "encoded by ATG"
XX FT Misc-difference 59 /note= "encoded by CCN"
XX PN MO958569-A1.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99WO-AU00343.
XX PR 11-MAY-1998; 98AU-0003450.
XX PA (UYOU ) UNIV QUEENSLAND.
XX PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX PA (MASC/) MASI P P.
XX PA (LAVI/) LAVIN M F.
XX PA (GAFV/) GAFNEY P J.
XX PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
XX DR WPI; 2000-039073/03.
XX DR N-PSDB; AAZ29019.
XX PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX PT agents -
XX PS Claim 8c; Page 69; 112pp; English.
XX PS The present sequence is the Textillinin protein, Txln 3, that is a
XX CC single stage competitive inhibitor of plasmin. It is isolated from the
XX CC Australian brown snake, Pseudonaja textilis textilis. It has six
XX CC conserved cysteine residues, that endow them great stability. This
XX CC sequence has haematopoietic and cytosolic activity. Txln has high
XX CC specificity for plasmin and low inhibitory efficiency, that can
XX CC transiently affect the delicate balance between enzymes and inhibitors
XX CC of the fibrinolytic system, controlling the fluidity of blood. The
XX CC plasmin inhibitors are useful for alleviating blood loss, following
XX CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX CC propensity to cause thrombosis.
XX SQ Sequence 59 AA;
XX Query Match 53.6%; Score 245; DB 21; Length 59;
XX Best Local Similarity 67.8%; Pred. No. 1.4e-21;
XX Matches 40; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

OY 25 KDRPFCLEPADTGPCRVFPSPFYNNPDEKCLBFIYGGCEGNANNFITKECESTCA 83
DB 1 KDRPFCLEPADTGPCRVFPSPFYNNPDEKCLBFIYGGCEGNANNFITKECESTCA 59

RESULT 13
AAY15143
ID AAY15143 standard; Protein; 59 AA.
XX AC AAY15143;
XX DT 07-FEB-2000 (first entry)

```

XX Txln 6 Plasmin inhibitor protein.
 XX Textilin protein; Txln 6; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX MO9958569-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFV/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 PI WPI: 2000-039073/03.
 DR N-PSDB; AA229022.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Claim 8f; Page 69; 112pp; English.
 PS
 XX The present sequence is the Textilin protein, Txln 6, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytoskeletal activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 XX Sequence 59 AA;
 SQ
 Query Match 49.7%; Score 227; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 1.9e-19;
 Matches 40; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 Oy 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCLRFYGGCGGNANNFTKECESTCAA 83
 Db 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCLRFYGGCGGNANNFTKECESTCAA 59
 ID AAY15142 standard; Protein; 59 AA.
 XX AAY15142;
 AC AAY15142;
 DT 07-FEB-2000 (first entry)
 XX Txln 5 Plasmin inhibitor protein.
 DE Textilin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM reduced propensity; thrombosis.

KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.
 OS
 XX MO9958569-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-AU00343.
 XX 11-MAY-1998; 98AU-0003450.
 XX (UYOU) UNIV QUEENSLAND.
 XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFV/) GAFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 PI WPI: 2000-039073/03.
 DR N-PSDB; AA229021.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Claim 8e; Page 69; 112pp; English.
 PS
 XX The present sequence is the Textilin protein, Txln 5, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytoskeletal activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 XX Sequence 59 AA;
 SQ
 Query Match 49.5%; Score 226; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 2.5e-19;
 Matches 40; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 Oy 25 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCLRFYGGCGGNANNFTKECESTCAA 83
 Db 1 KDRPFCFLPADTGPCRVRFPSFYNNPDEKCLRFYGGCGGNANNFTKECESTCAA 59
 ID AAY15141 standard; Protein; 59 AA.
 XX AAY15141;
 AC AAY15141;
 DT 07-FEB-2000 (first entry)
 XX Txln 4 Plasmin inhibitor protein.
 DE Textilin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytoskeletal activity; specificity; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX Pseudonaja textilis textilis.

XX	MO958569-A1.
PD	18-NOV-1999.
XX	
XX	07-MAY-1999; 99WO-AU00343.
XX	
PR	11-MAY-1998; 98AU-0003450.
XX	
PA	(UYQU) UNIV QUEENSLAND.
PA	(NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA	(MASC/) MASC P P.
PA	(LAVI/) LAVIN M P.
PA	(GAF/) GAFFNEY P J.
XX	
PI	Masci PP, Lavin MP, Gaffney PJ, Sorokina NI, Filippovich IV;
XX	
DR	WPI: 2000-039073/03.
DR	N-PSDB; AAZ29020.
XX	
PT	Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT	agents -
XX	
PS	Claim 8d; Page 69; 112pp; English.
XX	
CC	The present sequence is the Textillin protein, Txln 4, that is a
CC	single stree competitive inhibitor of plasmin. It is isolated from the
CC	Australian brown snake, Pseudonaja textilis textilis. It has six
CC	conserved cysteine residues, that endow them great stability. This
CC	sequence has haematopoietic and cytostatic activity. Txln has high
CC	specificity for plasmin and low inhibitory efficiency, that can
CC	transiently affect the delicate balance between enzymes and inhibitors
CC	of the fibrinolytic system, controlling the fluidity of blood. The
CC	plasmin inhibitors are useful for alleviating blood loss, following
CC	major surgery or trauma. Conjugates of the plasmin inhibitor and an
CC	anti-fibrin antibody are useful as anti-tumour agents. They have reduced
CC	propensity to cause thrombosis.
XX	
50	Sequence 59 AA;

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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 5.40141 Seconds

(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179A-8

Sequence: 1 KDHKFCFLPAETGSCCKGNV.....CGNANNFKTIEBCKSTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224	65.5	61	1	IVB1_VIPAA
2	212	62.0	57	1	IVBT_NAJNA
3	212	62.0	65	1	IVB1_BUNPA
4	209	61.1	57	1	IVB2_NAJNI
5	207	60.5	57	1	IVB2_HEMMA
6	207	60.5	65	1	IVB3_VIPAA
7	192	56.1	58	1	IVBC_OPHIA
8	189	55.3	62	1	IVBT_ERIMA
9	186	54.4	60	1	IVB2_DABRU
10	184	53.8	62	1	IVB2_ANESU
11	178	52.0	57	1	IVBK_DENAN
12	178	52.0	57	1	IVBK_DENPO
13	172	50.3	55	1	CSTI_BOWMO
14	172	50.3	55	1	IVBE_DENPO
15	168	49.1	304	1	TRPI_MACMU
16	168	48.8	58	1	AXP1_ANTAF
17	167	48.5	55	1	ISHI_STOHB
18	166	48.5	302	1	TRPI_RAT
19	165	48.2	55	1	ISH2_STOHB
20	165	48.2	110	1	IBP_CARCR
21	165	48.2	300	1	TRPI_RABIT
22	164	48.0	58	1	ISIK_HELPO
23	161	47.1	304	1	TRPI_HUMAN
24	157	45.9	57	1	IVBC_NAJNA
25	157	45.9	306	1	TRPI_MOUSE
26	155	45.3	58	1	AXP2_ANTAF
27	153	44.7	59	1	IVB1_DENAN
28	150	43.9	60	1	IVB1_DENPO
29	150	43.9	235	1	TRP2_HUMAN
30	149	43.6	230	1	TRP2_MOUSE
31	147	43.0	69	1	CRPT_BOOMI
32	146	42.7	102	1	ELAC_TRIUV
33	144.5	42.3	197	1	MCPI_MELCP

34	143	41.8	100	1	BPT1_BOVIN
35	143	41.8	507	1	SPT1_MOUSE
36	141	41.2	60	1	IBPS_BOVIN
37	141	41.2	60	1	TXCA_DENAN
38	141	41.2	763	1	APP2_HUMAN
39	140	40.9	57	1	IVBB_DENPO
40	140	40.9	351	1	TKD1_BOVIN
41	139	40.6	770	1	A4_MOUSE
42	138	40.4	100	1	BPT2_BOVIN
43	138	40.4	765	1	APP2_RAT
44	137	40.1	76	1	A4_MACMU
45	137	40.1	252	1	SPT2_HUMAN

ALIGNMENTS

RESULT 1	IVB1_VIPAA	STANDARD;	PRT;	61 AA.
AC	P00991;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom basic protease inhibitor I (Venom trypsin inhibitor I).			
OS	Vipera ammodytes ammodytes (Western sand viper).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Chordata; Serpentes; Colubroidae;			
OC	Viperidae; Viperinae; Vipera.			
OX	NCBI_TaxID=8705;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RY	MEDLINE=84053385; PubMed=6639951;			
RA	Rictonja A., Meloun B., Gubensek P.;			
RT	"The primary structure of Vipera ammodytes venom trypsin inhibitor			
RT	I."			
RL	Biochim. Biophys. Acta 748:429-435 (1983).			
CC	- FUNCTION: This protein inhibits trypsin and kallikrein.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- STRUTLARTY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	PIR; A01222; TIVITI.			
DR	HSSP; P31713; ISHP.			
DR	Inceprp; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI_1.			
DR	Pfam; PF000222; Kunitz_BPTI_1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
KW	PROSITE; PS0279; BPTI_KUNITZ_2; 1.			
FT	Serine protease inhibitor; Pyroglutamate carboxylic acid.			
FT	MOD RES 1 57			
FT	DISULFD 7 57			
FT	DISULFD 16 40			
FT	DISULFD 32 53			
SO	SEQUENCE 61 AA; 6865 MW; FC8285F579FE3795 CRC64;			
Query Match	65.5%; Score 224; DB 1; Length 61;			
Best Local Similarity	62.7%; Pred. No. 7.2e-20;			
Matches	37; Conservative 10; Mismatches 12; Indels 0;			
Oy	1 KDHKFCFLPAETGSCCKGNVPRFYNNADHOCLEKFIYGGCGNANNFKTIEBCKSTCAA 59			
Db	1 QDHKFCFLPADPGRCKAHIRFTYDSASNCKNKRTIYGGCGNANNFKTIEWDCROTGA 59			
RESULT 2	IVBT_NAJNA	STANDARD;	PRT;	57 AA.
AC	P20229;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom trypsin inhibitor.			

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OS Naja naja (Indian cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
NCBI_TaxID=35670;
OK NCB1 (1)
RN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91099304; Pubmed=1702708;
RA Shafiqat J., Beg O.U., Yin S.-J., Zaidi Z.H., Joernvall H.;
RT "Primary structure and functional properties of cobra (Naja naja
naia) venom Kunitz-type trypsin inhibitor.";
RL Eur. J. Biochem. 194;337-341(1990).
CC -1- FUNCTION: This protein inhibits trypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR, S13846; S13846.
DR HSSP, P00981; 1DTX.
DR InterPro, IPR002223; Kunitz_BPTI.
DR Pfam, PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom, PD000222; Kunitz_BPTI; 1.
DR SMART, SM00131; KU; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE, PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6371 MW; AABPD72949ADCL2A CRC64;

Query Match 62.0%; Score 212; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 1,7e-18;
Matches 36; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 PKFCELPARTGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 57
DB 2 PKFCELPARTGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 55

RESULT 3
IYB1_BUNFA STANDARD; PRT; 65 AA.
AC P25660;
DT 01-MAY-1992 (Rel. 22, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitors IX and VIIIB.
OS Bungarus fasciatus (Banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
NCBI_TaxID=8613;
OK NCB1 (1)
RN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=83160048; Pubmed=6832893;
RA Liu C.-S., Wu T.-C., Lo T.-B.;
RT "Complete amino acid sequences of two protease inhibitors in the
venom of Bungarus fasciatus.";
RL Int. J. Pept. Protein Res. 21:209-215(1983).
CC -1- FUNCTION: Inhibitor of chymotrypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP, P00980; 1DTX.
DR InterPro, IPR002223; Kunitz_BPTI.
DR Pfam, PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom, PD000222; Kunitz_BPTI; 1.
DR SMART, SM00131; KU; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_2; 1.
DR PROSITE, PS00279; BPTI_KUNITZ_2; 1.

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KW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 63 65 MISSING (IN INHIBITOR VIIIB).
SQ SEQUENCE 65 AA; 7294 MW; BA340749E194DB51 CRC64;

Query Match 62.0%; Score 212; DB 1; Length 65;
Best Local Similarity 62.7%; Pred. No. 2e-18;
Matches 37; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 KDPKCELPARTGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTCA 59
DB 1 KNPPTCNILPRTGRGNALIPAFYNSHLKCKFYGGCGGANNFKTIEBKGSTCA 59

RESULT 4
IYB2_NAJNI STANDARD; PRT; 57 AA.
AC P00986;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II.
OS Naja naja (Cape cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
NCBI_TaxID=8655;
OK NCB1 (1)
RN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76237547; Pubmed=950337;
RA Hokana Y., Iwanaga S., Tatsuki T., Suzuki T.;
RT "Snake venom protease inhibitors. III. Isolation of five
RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
(Ringhals cobra) and Naja naja (Cape cobra) and the complete amino
RT acid sequences of two of them.";
RL J. Biochem. 79:559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is probably similar to
that of bovine basic protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP, P00981; 1DTX.
DR InterPro, IPR002223; Kunitz_BPTI.
DR Pfam, PF00014; Kunitz_BPTI; 1.
DR ProDom, PD000222; Kunitz_BPTI; 1.
DR SMART, SM00131; KU; 1.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE, PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

Query Match 61.1%; Score 209; DB 1; Length 57;
Best Local Similarity 66.7%; Pred. No. 3.9e-18;
Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 4 PKFCELPARTGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 57
DB 2 PKFCELPARTGCKGNVPRFYNNADHHQCKLFYGGCGGANNFKTIEBKGSTC 55

RESULT 5
IYB2_HEMHA STANDARD; PRT; 57 AA.
AC P00985;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Hemachatus haemachatus (Ringhale) (sepedon haemachatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Elapidae; Elapinae; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC NCBI_TaxID=8626;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=6237547; PubMed=950337;
 RA Hokana Y., Iwanaga S., Tatsuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Ringhale's cobra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them."
 RL J. Biochem. 79:559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is similar to that of
 CC bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01216; TIRIV2.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6407 MW; 37CF03D3A03D7E2A CRC64;
 Query Match 60.5%; Score 207; DB 1; Length 57;
 Best Local Similarity 66.7%; Pred. No. 6.7e-19;
 Matches 36; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
 QY 4 PKFCELPALPAGTSCGKGVPRFYNNADHQCLEFIYGGCGGNANFKTIEGKSTC 57
 Db 2 PKFCELPALPAGTSCGKGVPRFYNNADHQCLEFIYGGCGGNANFKTIEGKSTC 55
 RESULT 6
 ID IVB3 VIPAA STANDARD; PRT; 65 AA.
 AC P00952;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).
 OS Viperidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Viperinae; Viperinae;
 OC NCBI_TaxID=8705;
 RN [1]
 RP SEQUENCE
 RX TISSUE=Venom;
 RA Ritonja A., Meloun B., Gubensek F.;
 RT "The primary structure of Viperinae venom chymotrypsin
 RT inhibitor."
 RL Biochim. Biophys. Acta 746:138-145(1983).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01223; TIVIVC.
 DR HSSP; P31713; ISHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT SITE 17 18
 SQ SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7CC57 CRC64;
 Query Match 60.5%; Score 207; DB 1; Length 65;
 Best Local Similarity 61.0%; Pred. No. 7.7e-19;
 Matches 36; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
 QY 1 KDHPKCELPALPAGTSCGKGVPRFYNNADHQCLEFIYGGCGGNANFKTIEGKSTCA 59
 Db 1 KDHPKCELPALPAGTSCGKGVPRFYNNADHQCLEFIYGGCGGNANFKTIEGKSTCA 59
 RESULT 7
 ID IVBC OPHNA STANDARD; PRT; 58 AA.
 AC P82966;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom chymotrypsin inhibitor.
 OS Ophiophagus hannah (King cobra) (Naja hannah).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Elapidae; Elapinae; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC NCBI_TaxID=8665;
 RN [1]
 RP SEQUENCE
 RX TISSUE=Venom gland;
 RX MEDLINE=21248396; PubMed=11350064;
 RA Chang L.-S., Chung C., Huang H.-B., Lin S.-R.;
 RT "Purification and characterization of a chymotrypsin inhibitor from
 RT the venom of Ophiophagus hannah (King Cobra)."
 RL Biochem. Biophys. Res. Commun. 283:862-867(2001).
 CC -1- FUNCTION: This protein inhibits chymotrypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P00981; IDTK.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IDA.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 6 56 BY SIMILARITY.
 FT DISULFID 15 39 BY SIMILARITY.
 FT DISULFID 31 52 BY SIMILARITY.
 FT ACT SITE 16 17 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 58 AA; 6499 MW; 3EB44C85F0843D8A CRC64;
 Query Match 56.1%; Score 192; DB 1; Length 58;
 Best Local Similarity 63.0%; Pred. No. 4e-16;
 Matches 34; Conservative 2; Mismatches 18; Indels 0; Gaps 0;
 QY 4 PKFCELPALPAGTSCGKGVPRFYNNADHQCLEFIYGGCGGNANFKTIEGKSTC 57
 Db 3 PKFCELPALPAGTSCGKGVPRFYNNADHQCLEFIYGGCGGNANFKTIEGKSTC 56
 RESULT 8
 ID IVBT ERIMA STANDARD; PRT; 62 AA.
 AC P24511;

DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis machanoni (leaf-nosed viper).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Viperinae; Eristocophis.
 OX NCBI_TaxID=8702;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=92077130; PubMed=1743283;
 RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 from leaf-nosed viper venom."
 RL FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: S19327; S19327.
 DR HSSP; P00981; 1DPTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR Kunitz-type trypsin inhibitor.
 FT DISULFID 2 52 BY SIMILARITY.
 FT DISULFID 11 35 BY SIMILARITY.
 FT ACT SITE 27 48 BY SIMILARITY.
 FT ACT SITE 12 13 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0AD20DF938 CRC64;

Query Match 55.3%; Score 189; DB 1; Length 62;
 Best Local Similarity 59.3%; Pred. No. 9, 6e-16;
 Matches 32; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 6 FCELPATGSCGVNPRFYTNADHOCLEKFTYGGCGGANNFTIEGKSTCA 59
 DB 1 FCELPDPCVCAHIFRFTYTNADHOCLEKFTYGGCGGANNFTIEGKSTCA 54
 [1]
 RESULT 9
 IYB2_DABRU STANDARD; PRT; 60 AA.
 AC P00950;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II (RVV-II).
 OS Daboia russelii stanselii (Siamese Russell's viper) (Vipera russelii
 siamensis).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Viperinae; Daboia.
 OX NCBI_TaxID=8708;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=75060360; PubMed=4436285;
 RA Takahashi H., Iwanaga S., Kitagawa T., Hokama Y., Suzuki T.;
 RT "Snake venom proteinase inhibitors. II. Chemical structure of
 inhibitor II isolated from the venom of Russell's viper (Vipera
 russelii)." ;
 RL J. Biochem. 76:721-733(1974).
 CC -1- FUNCTION: This inhibitor has activity similar to bovine basic
 protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR HSSP; P10646; 1ADZ.

DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRODOM; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR Kunitz-type trypsin inhibitor.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT ACT SITE 17 18
 SQ SEQUENCE 60 AA; 6850 MW; 5A7DCE9554CB6A2 CRC64;

Query Match 54.4%; Score 186; DB 1; Length 60;
 Best Local Similarity 53.6%; Pred. No. 2, 1e-15;
 Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 DHPKFCBIPATGSCGVNPRFYTNADHOCLEKFTYGGCGGANNFTIEGKSTC 57
 DB 2 DRPFCNLAPEBGRGRHLRIYTNLESNCKKVFYGGCGGANNFTIEGKSTC 57
 [1]
 RESULT 10
 IYB2_ANESU STANDARD; PRT; 62 AA.
 AC P10280;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protease inhibitor 5 II (SAS II).
 OS Anemona sulcata (Snake-loose sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 CC Nymanthea; Actinidae; Anemona.
 OX NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE OF 1-59.
 RA Wunderer G., Machleidt W., Fritz H.;
 RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
 Anemona sulcata."
 RL Meth. Enzymol. 80:816-820(1981).
 RN [2]
 RP SEQUENCE.
 RA Krebs H.C., Habermehl G.G.;
 RT "Isolation and structural determination of a hemolytic active peptide
 from the sea anemone Metridium senile."
 RL Naturwissenschaften 74:395-396(1987).
 CC -1- FUNCTION: INHIBITOR OF KALLIKREIN.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S07451; S07451.
 DR HSSP; P11713; 1SHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR Serine protease inhibitor.
 FT DISULFID 5 55
 FT DISULFID 14 38
 FT DISULFID 30 51
 FT ACT SITE 15 16
 FT VARIANT 13 13 A -> R.
 FT VARIANT 16 16 A -> G.
 FT VARIANT 17 17 S -> G.
 FT VARIANT 25 25 S -> L.
 FT VARIANT 28 28 K -> R.
 FT VARIANT 39 39 G -> R.
 SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 53.8%; Score 184; DB 1; Length 62;
 Best Local Similarity 58.8%; Pred. No. 3, 7e-15;
 Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

OY 7 CELPAAETGSCKGNVPRFYNNADHHQCLKFIYGGCGGNANFKTIEEGKSTC 57
 DB 5 CELPKVGVPCGARRPRRYNNSSSKRCCEFIYGGCGGNANFKTIEEGKSTC 55

RESULT 11
 IYBK_DENAN STANDARD; PRT; 57 AA.
 AC P00982;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor K (Dendrotoxin delta-DatX) (Toxin
 DE C131C3).
 OS Dendroaspis angusticeps (Eastern green mamba).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8618;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81045446; PubMed=7429422;
 RA Joubert F.J., Taljaard N.;
 RT "Snake venoms. The amino acid sequences of two proteinase inhibitor
 RT homologues from Dendroaspis angusticeps venom."
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:661-674(1980).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=88318591; PubMed=2457792;
 RA Benishin C.G., Sorensen R.G., Brown W.E., Krueger B.K.,
 RA Blaustein M.P.;
 RT "Four polypeptide components of green mamba venom selectively block
 RT certain potassium channels in rat brain synaptosomes."
 RL Mol. Pharmacol. 34:152-159(1988).
 CC -1- FUNCTION: This protease inhibitor homolog has very low toxicity.
 CC It blocks voltage-gated potassium channels and facilitate
 CC neurotransmitter release.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: LD(50) is 15 mg/kg by intravenous injection.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: A91691; TIEPVA.
 DR HSSP: P00981; IDTK.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI_1.
 DR ProDom: PD000222; Kunitz_BPTI_1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Toxin; Neurotoxin;
 KW Potassium channel inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SO SEQUENCE 57 AA; 6574 MW; A4070CBB141DB3 CRC64;

Query Match 52.0%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 1.7e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 5 KCELPAAETGSCKGNVPRFYNNADHHQCLKFIYGGCGGNANFKTIEEGKSTC 57
 DB 3 KYCKPLRIGPCGARRPRRYNNSSSKRCCEFIYGGCGGNANFKTIEEGKSTC 55

RESULT 12
 IYBK_DENPO STANDARD; PRT; 57 AA.
 AC P00981;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Venom basic protease inhibitor K (Dendrotoxin K).
 OS Dendroaspis polylepsis polylepsis (Black mamba).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8620;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=77158069; PubMed=857902;
 RA Strydom D.J.;
 RT "Snake venom toxins. The amino acid sequence of toxin Vi2, a
 RT homologue of pancreatic trypsin inhibitor, from Dendroaspis polylepsis
 RT polylepsis (black mamba) venom."
 RL Biochim. Biophys. Acta 491:361-369(1977).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94076347; PubMed=8254670;
 RA Berndt K.D., Guentert P., Wuehrlich K.;
 RT "Nuclear magnetic resonance solution structure of dendrotoxin K from
 RT the venom of Dendroaspis polylepsis polylepsis."
 RL J. Mol. Biol. 234:735-750(1993).
 CC -1- FUNCTION: This protein is much less toxic to mice than is whole
 CC venom. It inhibits trypsin slightly, but chymotrypsin not at all.
 CC It is a highly selective blocker of voltage-gated potassium
 CC channels.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: LD(50) IS 30 MG/KG BY INTRAVENOUS INJECTION.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PDB: IDTK; 3I-VAN-94.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI_1.
 DR ProDom: PD000222; Kunitz_BPTI_1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
 KW 3D-structure; Potassium channel inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 FT STRAND 18 24
 FT TURN 25 28
 FT STRAND 29 35
 FT STRAND 45 45
 FT HELIX 48 55
 SO SEQUENCE 57 AA; 6566 MW; C30818FB3C41CB87 CRC64;

Query Match 52.0%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 1.7e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 5 KCELPAAETGSCKGNVPRFYNNADHHQCLKFIYGGCGGNANFKTIEEGKSTC 57
 DB 3 KYCKPLRIGPCGARRPRRYNNSSSKRCCEFIYGGCGGNANFKTIEEGKSTC 55

RESULT 13
 CSTI_BOMMO STANDARD; PRT; 55 AA.
 AC P81902;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
 OS Bombyx mori (Silk moth).
 OC Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyota; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]

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RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Asahi;
RX MEDLINE=99115431; PubMed=9914483;
RA Kuritoka A., Yamazaki M., Hirano H.;
RT "Primary structure and possible functions of a trypsin inhibitor of
  Bombus morio.";
RL Eur. J. Biochem. 259:120-126(1999).
CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
CC activity by forming a low-dissociation complex with trypsin. May
CC play an important part in regulating proteolytic activity in the
CC silk gland or protecting silk proteins from degradation during
CC histolysis.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
CC gland.
CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
CC middle silk glands during the final stage of larval growth with
CC highest expression before the onset of spinning.
CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
CC -1- MISCELLANEOUS: Has an isoelectric point of 4.3.
CC -1- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR HSSP; P31713; 1SRP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR KMW Developmental protein; Serine protease inhibitor.
FT DISULFID 4 54 BY SIMILARITY.
FT DISULFID 13 37 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT ACT_SITE 14 15 REACTIVE BOND (TRYPSIN) (BY
SQ SEQUENCE 55 AA; 6027 MW; C2739B8B72BB6E59 CRC64;

Query Match 50.3%; Score 172; DB 1; Length 55;
Best Local Similarity 54.9%; Pred. No. 8.5e-14;
Matches 28; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 7 CELPAETSGKGNVPRFYNDADHOCLEKFIYGGCGGANNFTIEGKSTC 57
DB 4 CLLPKTPCKSGSPRYAVDSSEDCVETRYGCGQANNFTIECEAC 54

RESULT 14
IYBE_DENPO STANDARD; PRT; 59 AA.
ID IYBE_DENPO
AC P00984;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Venom basic protease inhibitor B (Dendrocoxin B).
OS Dendroaspis polylepis polylepis (Black Mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Dendroaspis.
CC NCBI_TaxID=8620;
RX NCBI [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=78214615; PubMed=666688;
RA Joubert F.J., Strydom D.J.;
RT "Snake venoms. The amino-acid sequence of trypsin inhibitor B of
  Dendroaspis polylepis polylepis (Black Mamba) venom.";
RL Eur. J. Biochem. 87:191-196(1978).
CC -1- FUNCTION: This protein inhibits trypsin and binds transition metal
CC ions such as copper and cobalt.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01215; TIEPED.
DR HSSP; P00981; LDTK.

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DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR KMW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT_SITE 17 18 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 59 AA; 6620 MW; B87BFBECC090276 CRC64;

Query Match 50.3%; Score 172; DB 1; Length 59;
Best Local Similarity 54.5%; Pred. No. 9.1e-14;
Matches 30; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 3 HPKCELPATSGKGNVPRFYNDADHOCLEKFIYGGCGGANNFTIEGKSTC 57
DB 3 HTPFKLPATSGKGNVPRFYNDADHOCLEKFIYGGCGGANNFTIEGKSTC 57

RESULT 15
IYBE_DENPO STANDARD; PRT; 304 AA.
ID IYBE_DENPO
AC IYBE_DENPO
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
  associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
  (EPI).
FT TFP1 OR TFP11.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
CC NCBI_TaxID=9544;
CC NCBI [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94375417; PubMed=8089087;
RA Kamei S., Kamikubo Y., Hamuro T., Fujimoto H., Ishihara M.,
  Yonemura H., Miyamoto S., Funatsu A., Enjoji K., Abumaya T.;
RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue
  factor pathway inhibitor (TFPI): comparison with human TFPI.";
RL J. Biochem. 115:708-714(1994).
CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
  WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY. PRESUMABLY BY FORMING
  A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
  ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
  LIPOPROTEINS IN PLASMA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
CC -----
DR EMBL; S73317; AAB31955.1; -
DR PIR; JC2264; JC2264.
DR HSSP; P10646; ITRX.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 3.
DR SMART; SM00131; KU; 3.

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DR PROSITE; PS00280; BPTI KUNITZ 1; 3.
 DR PROSITE; PS50279; BPTI KUNITZ 2; 3.
 KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
 KW Signal.

FT	SIGNAL	1	28	BY SIMILARITY.
FT	CHAIN	29	304	TISSUE FACTOR PATHWAY INHIBITOR.
FT	DOMAIN	54	104	BPTI/KUNITZ INHIBITOR 1
FT	DOMAIN	125	175	(VII (A)/TISSUE FACTOR BINDING SITE).
FT	DOMAIN	125	175	BPTI/KUNITZ INHIBITOR 2
FT	DOMAIN	125	175	(FACTOR X(A) BINDING SITE).
FT	DOMAIN	125	175	BPTI/KUNITZ INHIBITOR 3.
FT	DOMAIN	217	267	BY SIMILARITY.
FT	DISULFID	54	104	BY SIMILARITY.
FT	DISULFID	63	87	BY SIMILARITY.
FT	DISULFID	79	100	BY SIMILARITY.
FT	ACT SITE	64	65	REACTIVE BOND (BY SIMILARITY).
FT	DISULFID	125	175	BY SIMILARITY.
FT	DISULFID	134	158	BY SIMILARITY.
FT	DISULFID	150	171	BY SIMILARITY.
FT	ACT SITE	135	136	REACTIVE BOND (BY SIMILARITY).
FT	DISULFID	217	267	BY SIMILARITY.
FT	DISULFID	226	250	BY SIMILARITY.
FT	DISULFID	242	263	BY SIMILARITY.
FT	ACT SITE	227	228	REACTIVE BOND (BY SIMILARITY).
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	256	256	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	304 AA;	35085 MM;	56E13B3FP1628280 CRC64;

Query Match 49.1%; Score 168; DB 1; Length 304;
 Best Local Similarity 49.1%; Pred. No. 1.3e-12;
 Matches 28; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

OY 1 KDHKFCFCELPATGSCGKGNVPRFYADHQCLEKFTYGGCGGANNPKTIEGKSTC 57
 DB 119 QEKPDPCFLIEDPFCICRGYITRYFYNNQSKQCRFRKYGGCLGNMNPETLECKNTC 175

Search completed: January 23, 2004, 10:25:14
 Job time : 5.40141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:23 ; Search time 9.14085 Seconds

(without alignments)
620.725 Million cell updates/sec

Title: US-09-700-179A-8

Perfect score: 342
Sequence: 1 KDHPKCELPAPETGSCCKGNV.....CGGNANFKTIEBKSTCA 59Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	224	65.5	61	1	TIYVTT1
2	212	62.0	57	2	S13846
3	209	61.1	57	1	TINMVC
4	207	60.5	57	1	TIYVVC
5	207	60.5	65	1	TIYVVC
6	202	59.1	62	2	A44180
7	189	55.3	62	2	TIYVVC
8	186	54.4	60	1	TIYVVC
9	184	53.8	62	2	S07451
10	178	52.0	57	1	TIYVVC
11	178	52.0	79	1	TIYVVC
12	174	50.3	57	2	A59204
13	172	50.3	57	2	B59399
14	172	50.3	59	1	TIYVVC
15	172	50.3	59	1	TIYVVC
16	168	49.1	304	2	A59399
17	166	48.5	55	2	S10332
18	166	48.5	302	1	TIYVVC
19	165	48.2	110	1	TIYVVC
20	165	48.2	299	2	I46937
21	165	48.2	300	2	S12143
22	164	48.0	58	1	TIYVVC
23	161	47.1	304	1	TIYVVC
24	157	45.9	57	2	S12957
25	156	45.6	396	2	S53325
26	154	45.0	1558	2	C89114
27	154	45.0	2167	2	T34395
28	153	44.7	59	1	TIYVVC
29	152	44.4	249	2	T32060

30	150	43.9	60	1	TIYVVC	venom basic protei
31	150	43.9	235	2	A54951	tissue factor path
32	146	42.7	102	2	S69288	early lactation pr
33	146	42.7	2225	2	T26063	hypothetical prote
34	144	42.1	805	2	T34212	hypothetical prote
35	143	41.8	59	2	S00371	isoprotein G1 -
36	143	41.8	100	1	TIYVVC	basic proteinase 1
37	143	41.8	111	2	S41082	amyloid precursor
38	143	41.8	747	2	U07773	Alzheimer's diseas
39	141	41.2	58	2	S10063	isoprotein G2 -
40	141	41.2	60	1	TIYVVC	serum basic protei
41	141	41.2	60	2	A36989	calcitriol - eas
42	141	41.2	751	2	A49974	beta-amyloid precu
43	141	41.2	763	2	A49321	amyloid beta (A4)
44	140	40.9	57	1	TIYVVC	venom basic protei
45	139	40.6	76	2	S04855	Alzheimer's diseas

ALIGNMENTS

RESULT 1

TIYVTT1
venom basic proteinase inhibitor I - western sand viper

N/Alternate names: venom trypsin inhibitor I

C/Species: Viper a ammodytes ammodytes (western sand viper)

C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996

C/Accession: A01222

R/Rittonja, A.; Meloun, B.; Gubensek, F.

Biochim. Biophys. Acta 748, 429-435, 1983

A/Title: The primary structure of Viper a ammodytes venom trypsin inhibitor I.

A/Reference number: A01222; PMID:84053385; PMID:6639951

A/Accession: A01222

A/Molecule type: protein

A/Residues: 1-61 <RIT>

C/Comment: This protein inhibits trypsin and kallikrein.

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C/Keywords: pyroglutamic acid; serine proteinase inhibitor; venom

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

F/7-57,16-40,32-53/Diulfide bonds: #status predicted

F/17/inhibitory site: Lys (trypsin) #status predicted

Query Match 65.5%; Score 224; DB 1; Length 61;
Best local Similarity 62.7%; Pred. No. 1.5e-19;
Matches 37; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 KDHPKCELPAPETGSCCKGNVPRFYVADHHCCKFTYGGCGGNANFKTIEBKSTCA 59

Db 1 QDHPKCELPAPETGSCCKGNVPRFYVADHHCCKFTYGGCGGNANFKTIEBKSTCA 59

RESULT 2

S13846
venom animal Kunitz-type trypsin inhibitor - Indian cobra

C/Species: Naja naja naja (Indian cobra)

C/Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000

C/Accession: S13846

R/Shafiqat, U.; Beg, O.U.; Yin, S.J.; Zaidi, Z.H.; Joernvall, H.

Eur. J. Biochem. 194, 337-341, 1990

A/Title: Primary structure and functional properties of cobra (Naja naja) venom K

A/Reference number: S13846; PMID:91099304; PMID:1702708

A/Accession: S13846

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <SNA>

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C/Keywords: serine proteinase inhibitor; venom

F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 62.0%; Score 212; DB 2; Length 57;
Best local Similarity 66.7%; Pred. No. 3.6e-18;
Matches 36; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Biochim. Biophys. Acta 746, 138-145, 1983

6. EGGI DAEFGCCVKNR/DPEYVNA DHHC1.KPTVGCGGNANFEKTIREGKSTCA 59

6 FCELPATGSCKNVPRFYNNADHQCLKFIYGGCGGNANPEXTIEEGKTCOA 59

Db 1 FCVLPDDPGVCKAHPFRYYNPASNKCNPIYGGCGGANNPFRACRHTCVA 54

RESULT 8

TIIEPV2

venom basic proteinase inhibitor II - Russell's viper

C/Species: Vipera russelli (Russell's viper)

C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C/Accession: A01221

R./Accession: A01221

J./Accession: A01221

A./Title: Snake venom proteinase inhibitor. II. Chemical structure of inhibitor II

A./Reference number: A01221; PMID:75060360; PMID:4436285

A./Accession: A01221

A./Molecule type: protein

A./Residues: 1-60 <TAK>

C/Comment: This inhibitor has activity similar to that of bovine basic protease inhibitor

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F./5-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F./7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 54.4%; Score 186; DB 1; Length 60;
 Best Local Similarity 53.6%; Pred. No. 4,4e-15;
 Matches 30; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Oy 2 DHPKCELPARTGSCGNVPRFYNNADHHQCLKPIYGGCGGANNFKTIEBGKSTC 57
 Db 2 DRPTFCNLAPSGRCRHLRRIYYNLBSNCKCVFYGGCGGANNFETDECRCTC 57

RESULT 9

S07451

proteinase inhibitor 5.II - snake-locks sea anemone

C/Species: Anemonia sulcata (snake-locks sea anemone)

C/Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997

C/Accession: S07451; B27222

R./Accession: S07451; B27222

R./Munderer, G.; Machleidt, W.; Fritz, H.

Meth. Enzymol. 80, 816-820, 1981

A./Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia

A./Reference number: S07451

A./Accession: S07451

A./Molecule type: protein

A./Residues: 1-59 <MUN>

A./Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found

R./Krebs, H.C.; Habermehl, G.G.

Naturwissenschaften 74, 395-396, 1987

A./Title: Isolierung und strukturaufklärung eines haemolytisch aktiven peptids aus der

A./Reference number: A94700

A./Accession: B27222

A./Molecule type: protein

A./Residues: 1-38, 'R', '40', 'B', '42', 'BB', '45-48', 'Z', '51', 'Z', '53-62 <KRE>

C/Comment: This protein is much less toxic to mice than is whole venom. It inhibits tr

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor

F./5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 53.8%; Score 184; DB 2; Length 62;
 Best Local Similarity 58.8%; Pred. No. 7.9e-15;
 Matches 30; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Oy 7 CELPAPETGSCGNVPRFYNNADHHQCLKPIYGGCGGANNFKTIEBGKSTC 57
 Db 5 CELPVPVPCRRARPRYYNSSSKCEKPIYGGCGGANNFTIEBCRCVC 55

RESULT 10

TIIEPV2

venom basic proteinase inhibitor K - eastern green mamba

N/Alternate names: dendrotoxin delta-Darx

C/Species: Dendroaspis angusticeps (eastern green mamba)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997

C/Accession: A91691; C32508; A01213

R./Joubert, F.J.; Taljaard, N.
 Hoppe-Sevler's Z. Physiol. Chem. 361, 661-674, 1980
 A./Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroasp

A./Reference number: A91691; PMID:81045446; PMID:7429422
 A./Accession: A91691

A./Molecule type: protein

A./Residues: 1-57 <UOU>

R./Benishin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.

Mol. Pharmacol. 34, 152-159, 1988

A./Title: Four polypeptide components of green mamba venom selectively block certain pot

A./Reference number: A93137; PMID:88318591; PMID:2457792

A./Accession: C32508

A./Molecule type: protein

A./Note: the amino acid composition of the inhibitor is identical with that predicted in

C/Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: venom

F./5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F./5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 52.0%; Score 178; DB 1; Length 57;
 Best Local Similarity 58.5%; Pred. No. 3.7e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 5 KCELPARTGSCGNVPRFYNNADHHQCLKPIYGGCGGANNFKTIEBGKSTC 57
 Db 3 KYCKLPVATGCKKIPSFYKMKAKCKLPFYSGCGGANNFKTIEBCRRTC 55

RESULT 11

TIIEPV2

K+ channel blocker dendrotoxin K - black mamba

C/Species: Dendroaspis polylepsis polylepsis (black mamba)

C/Date: 30-Nov-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

C/Accession: A49291; A01213

R./Smith, L.A.; Lafaye, P.J.; Lapenotiere, H.F.; Spain, T.; Dolly, J.O.

Biochemistry 32, 5692-5697, 1993

A./Title: Cloning and functional expression of dendrotoxin K from black mamba, a K+ cha

A./Reference number: A49291; PMID:93277850; PMID:8504088

A./Accession: A49291

A./Status: preliminary

A./Molecule type: mRNA; protein

A./Residues: 1-79 <SMI>

A./Cross-references: GB:861886; NID:9385317; PID:AAB26998.1; PID:9385318

A./Note: sequence extracted from NCBI backbone (NCBI:133053, NCBI:133054)

A./Note: the source is designated as Dendroaspis polylepsis

R./Strydom, D.J.

Biochim. Biophys. Acta 491, 361-369, 1997

A./Title: Snake venom toxins. The amino acid sequence of toxin Vi2, a homologue of panc

A./Reference number: A90617; PMID:77158069; PMID:857992

A./Accession: A01213

A./Molecule type: protein

A./Residues: 23-79 <STR>

C/Comment: This protein is much less toxic to mice than is whole venom. It inhibits tr

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: venom

F./27-77/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F./27-77,36-60,52-73/Disulfide bonds: #status predicted

Query Match 52.0%; Score 178; DB 1; Length 79;
 Best Local Similarity 58.5%; Pred. No. 5.1e-14;
 Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 5 KCELPARTGSCGNVPRFYNNADHHQCLKPIYGGCGGANNFKTIEBGKSTC 57
 Db 25 KYCKLPVATGCKKIPSFYKMKAKCKLPFYSGCGGANNFKTIEBCRRTC 77

RESULT 12

A59204

basic proteinase inhibitor - great pond snail

N/Alternate names: trypsin inhibitor

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:18 ; Search time 28.4613 Seconds
(without alignments)
329.039 Million cell updates/sec

Title: US-09-700-179A-8

Perfect score: 342
Sequence: 1 KDHKPCFCELPATGSCCKGNV.....CGGNANNKTIIEGSKTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_19Jun03.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	342	100.0	59	21 AA15141 Txln 4 Plasmin inh
2	342	100.0	83	21 AA15148 Proform of Txln 4
3	256	74.9	59	21 AA15140 Txln 3 Plasmin inh
4	256	74.9	83	21 AA15147 Proform of Txln 3
5	225	65.8	59	21 AA15138 Txln 1 Plasmin inh
6	225	65.8	83	21 AA15145 Proform of Txln 1
7	218	63.7	60	21 AA15153 Plasmin inhibitor
8	217	63.5	59	21 AA15139 Txln 2 Plasmin inh
9	217	63.5	83	21 AA15146 Proform of Txln 2

10	211	61.7	58	17 AA899146
11	201	58.8	59	21 AA15142
12	201	58.8	83	21 AA15149
13	193	56.4	60	21 AA15154
14	192	56.1	59	21 AA15143
15	192	56.1	83	21 AA15150
16	192	56.1	83	21 AA62525
17	178	52.0	57	15 AA81911
18	170	50.3	58	16 AA878542
19	172	49.7	58	16 AA81915
20	168	49.1	304	14 AA842309
21	168	48.5	58	16 AA81892
22	166	48.5	58	17 AA89197
23	166	48.5	302	14 AA835001
24	166	48.5	302	17 AA888513
25	165	48.2	58	17 AA839195
26	164	48.0	58	14 AA839800
27	164	48.0	111	14 AA839807
28	162	47.4	58	17 AA89194
29	162	47.4	161	17 AA800017
30	162	47.4	291	24 AA848476
31	162	47.4	291	24 AA848478
32	162	47.1	71	13 AA837399
33	161	47.1	110	12 AA81145
34	161	47.1	111	14 AA839804
35	161	47.1	160	13 AA839804
36	161	47.1	183	12 AA81146
37	161	47.1	225	22 AA002971
38	161	47.1	256	12 AA81169
39	161	47.1	261	12 AA81171
40	161	47.1	262	12 AA81172
41	161	47.1	265	12 AA81170
42	161	47.1	276	17 AA892265
43	161	47.1	276	17 AA892012
44	161	47.1	276	18 AA810311
45	161	47.1	276	19 AA861535

ALIGNMENTS

RESULT 1
ID AA15141 standard; Protein; 59 AA.
AC AA15141;
DT 07-FEB-2000 (first entry)
DE Txln 4 Plasmin inhibitor protein.
KW Textilin protein; Txln 4; plasmin inhibitor; single stage inhibitor;
KW Australian brown snake; conserved cysteine residue; stability; control;
KW haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
KW fluidity of blood; allelic; blood loss; major surgery; trauma; enzyme;
KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
KW reduced propensity; thrombosis.
OS Pseudomaja textilis textilis.
PN WO9958569-A1.
PD 18-NOV-1999.
PF 07-MAY-1999; 99WO-AU00343.
PR 11-MAY-1998; 98AU-0003450.
XX (UYOU) UNIV QUEENSLAND.
XX (MAB1-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.
XX (GAFF/) GAFFNEY P J.

Apoerlin-like Kun
Txln 5 Plasmin inh
Proform of Txln 5
Plasmin inhibitor
Txln 6 Plasmin inh
Proform of Txln 6
Protease-inhibitor
Kallikrein inhibitor
Human Lact-K2 deri
Lacti gene product.
Kallikrein inhibit
Genetically engine
Lacti. Rattus rat
Lipoprotein-associ
Genetically engine
Kunitz-type protea
Synthetic yeast le
Genetically engine
TFPI chimeric prot
Human Tifepinix.
Human Tifepinix-A5
Lacti fragment 90 -
Ser-(Glu15-Thr161)
Synthetic yeast le
Lacti fragment 1 -
Ser-(Glu15-Thr161)
Angiotensin conver
Ser-(Asp1-Thr255)-E
Ser-(Asp1-Glu245)-
Ser-(Asp1-Ser248)-
Ser-(Asp1-Ile253)-
TFPI mutein, Lys36
TFPI mutein K36R.
Recombinant non-gl
Human tissue facto


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XX Maeci P, Lavin M, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI: 2000-039073/03.
XX N-PSDB: AA229020.
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 8d; Page 69; 112pp; English.
XX
XX The present sequence is the Textillin protein, Txln 4, that is a
XX single stage competitive inhibitor of plasmin. It is isolated from the
XX Australian brown snake, Pseudonaja textilis textilis. It has six
XX conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 59 AA;
SQ
XX
XX Query Match 100.0%; Score 342; DB 21; Length 59;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-35;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KDHPKFCBLPARGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 59
XX DB 1 KDHPKFCBLPARGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 59
XX
XX RESULT 2
XX ID AAY15148
XX AAY15148 standard; Protein; 83 AA.
XX
XX AC AAY15148;
XX
XX DT 07-FEB-2000 (first entry)
XX
XX DE Proform of Txln 4 protein.
XX
XX Textillin proform; Txln 4; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX FT /label= Leader_Peptide
XX FT 25..83
XX FT /label= Txln-4_protein
XX FT /note= "Textillin-4"
XX
XX WO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.

```

```

PA (GAFF/) GAFFNEY P J.
XX
XX Maeci P, Lavin M, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI: 2000-039073/03.
XX N-PSDB: AA229027.
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents -
XX
XX Claim 40d; Page 72; 112pp; English.
XX
XX The present sequence is the proform of the Textillin protein, Txln 4,
XX that is a single stage competitive inhibitor of plasmin. It is isolated
XX from the Australian brown snake, Pseudonaja textilis textilis. It has
XX six conserved cysteine residues, that endow them great stability. This
XX sequence has haematopoietic and cytostatic activity. Txln has high
XX specificity for plasmin and low inhibitory efficiency, that can
XX transiently affect the delicate balance between enzymes and inhibitors
XX of the fibrinolytic system, controlling the fluidity of blood. The
XX plasmin inhibitors are useful for alleviating blood loss, following
XX major surgery or trauma. Conjugates of the plasmin inhibitor and an
XX anti-fibrin antibody are useful as anti-tumour agents. They have reduced
XX propensity to cause thrombosis.
XX
XX Sequence 83 AA;
SQ
XX
XX Query Match 100.0%; Score 342; DB 21; Length 83;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-35;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 KDHPKFCBLPARGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 59
XX DB 25 KDHPKFCBLPARGSCCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEBGSCTCAA 83
XX
XX RESULT 3
XX ID AAY15140
XX AAY15140 standard; Protein; 59 AA.
XX
XX AC AAY15140;
XX
XX DT 07-FEB-2000 (first entry)
XX
XX DE Txln 3 Plasmin inhibitor protein.
XX
XX Textillin protein; Txln 3; plasmin inhibitor; single stage inhibitor;
XX Australian brown snake; conserved cysteine residue; stability; control;
XX haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
XX reduced propensity; thrombosis.
XX
XX Pseudonaja textilis textilis.
XX
XX WO9958569-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-AU00343.
XX
XX 11-MAY-1998; 98AU-0003450.
XX
XX (UYOU) UNIV QUEENSLAND.
XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX (MASC/) MASC P P.
XX (LAVI/) LAVIN M F.
XX (GAFF/) GAFFNEY P J.
XX
XX Maeci P, Lavin M, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI: 2000-039073/03.
XX N-PSDB: AA229019.

```

XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 8c; Page 69; 112pp; English.
 CC The present sequence is the Textillin protein, Txln 3, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 59 AA;
 XX
 Query Match 74.9%; Score 256; DB 21; Length 59;
 Best Local Similarity 71.2%; Pred. No. 1.4e-24;
 Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 KDHPKCELPARTGSCGNVPRFYNNADHOCLEKIYGGCGGANNFTIEBGSCTCA 59
 Db 1 KDRNPFCKLPARTGRCNAKIPRFYNNPRHOCIEFLYGGCGGANNFTIEBGSCTCA 59
 RESULT 4
 AAY15147
 ID AAY15147 standard; Protein; 83 AA.
 AC AAY15147;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Proform of Txln 3 protein.
 XX
 Textillin proform; Txln 3; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Leader_peptide
 FT 25..83
 FT /label= Txln-3 protein
 FT /note= "Textillinin-3"
 XX
 PN W09958569-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX MPI; 2000-039073/03.
 DR

DR N-PSDB; AA229026.
 XX
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 40c; Page 72; 112pp; English.
 CC The present sequence is the proform of the Textillin protein, Txln 3,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.
 CC
 SQ Sequence 83 AA;
 XX
 Query Match 74.9%; Score 256; DB 21; Length 83;
 Best Local Similarity 71.2%; Pred. No. 2e-24;
 Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 KDHPKCELPARTGSCGNVPRFYNNADHOCLEKIYGGCGGANNFTIEBGSCTCA 59
 Db 25 KDRNPFCKLPARTGRCNAKIPRFYNNPRHOCIEFLYGGCGGANNFTIEBGSCTCA 83
 RESULT 5
 AAY15138
 ID AAY15138 standard; Protein; 59 AA.
 AC AAY15138;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Txln 1 Plasmin inhibitor protein.
 XX
 Textillin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; homology; specificity; Aprotinin;
 KW Talcotoxin-associated plasmin inhibitor; Tac; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Leader_peptide
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 FT /label= Txln-3 protein
 FT /note= "Textillinin-3"
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 PN W09958569-A1.
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 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-AU00343.
 XX
 PR 11-MAY-1998; 98AU-0003450.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M P.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX MPI; 2000-039073/03.
 DR N-PSDB; AA229017.
 XX
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX

PS Claim 8a; Page 68; 112pp; English.

CC The present sequence is the Textillin protein, Txln 1, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln 1 has 45% and
 CC 58% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.

XX Sequence 59 AA;

Query Match 65.8%; Score 225; DB 21; Length 59;
 Best Local Similarity 67.8%; Pred. No. 1e-20;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 KDHPKCELPATGSCGNVPRPYNADHQCCKFTYGGCGGNANFKTIEGKSTCA 59
 DB 1 KDRPFCCLPADTGPCRVAFPSFYNNPDKCKLEFIYGGCGGNANFKTIEGKSTCA 59

RESULT 6

ID AAY15145
 AAY15145 standard; Protein; 83 AA.

AC AAY15145;

DT 07-FEB-2000 (first entry)

XX Proform of Txln 1 protein.

XX Textillin proform; Txln 1; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 XX haematopoietic; cytosolic activity; homology; specificity; control;
 XX Talcotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

OS Pseudonaja textilis textilis.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader_peptide
 FT Protein 25..83
 FT /label= Txln-1 protein
 FT /note= "Textillin-1"

XX WO958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

XX (GAFV/) GAFNEY P J.

XX Mascal PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV,
 DR WPI; 2000-039073/03.
 DR N-PSDB; AA229024.
 XX

PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -

PS Claim 40a; Page 71; 112pp; English.

XX The present sequence is the proform of the Textillin protein, Txln 1,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln 1 has 45% and
 CC 58% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.

XX Sequence 83 AA;

Query Match 65.8%; Score 225; DB 21; Length 83;
 Best Local Similarity 67.8%; Pred. No. 1.5e-20;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 KDHPKCELPATGSCGNVPRPYNADHQCCKFTYGGCGGNANFKTIEGKSTCA 59
 DB 25 KDRPFCCLPADTGPCRVAFPSFYNNPDKCKLEFIYGGCGGNANFKTIEGKSTCA 83

RESULT 7

ID AAY15153
 AAY15153 standard; Protein; 60 AA.

AC AAY15153;

DT 07-FEB-2000 (first entry)

XX Plasmin inhibitor Txln 1, encoded by partial cDNA sequence.

XX Textillin protein; Txln 1; plasmin inhibitor; single stage inhibitor;
 XX Australian brown snake; conserved cysteine residue; stability; control;
 XX haematopoietic; cytosolic activity; homology; specificity; enzyme;
 XX fluidity of blood; alleviate; blood loss; major surgery; trauma; cDNA;
 XX fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 XX inhibitory efficiency; reduced propensity; thrombosis.

XX Pseudonaja textilis textilis.

XX Key Location/Qualifiers
 FH Misc-difference 24
 FT /note= "encoded by TTG"
 FT Misc-difference 47
 FT /note= "encoded by GAT"
 FT Misc-difference 49
 FT /note= "encoded by ATG"

XX WO958569-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-AU00343.

XX 11-MAY-1998; 98AU-0003450.

XX (UYOU) UNIV QUEENSLAND.

XX (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.

XX (MASC/) MASC P P.

XX (LAVI/) LAVIN M F.

XX (GAFV/) GAFNEY P J.

XX Mascal PP, Lavin MF, Gafney PJ, Sorokina NI, Filippovich IV,
 DR WPI; 2000-039073/03.
 DR N-PSDB; AA229024.
 XX

DR WPI; 2000-039073/03.
 DR N-PSDB; AAZ29047.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 XX Disclousure; Fig 6; 112pp; English.
 CC The present amino acid sequence is the Txln 1, Textillin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for
 CC alleviating blood loss, following major surgery or trauma. Conjugates of
 CC the plasmin inhibitor and an anti-fibrin antibody are useful as
 CC anti-tumour agents. They have reduced propensity to cause thrombosis.
 CC
 SQ Sequence 60 AA;
 Query Match 63.7%; Score 218; DB 21; Length 60;
 Best Local Similarity 64.4%; Pred. No. 8e-20; Mismatches 15; Indels 0; Gaps 0;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 OY 1 KDHPKFCLELPATGSCGNVPRFYNNADHHQCLKFIYGGCGGANNFRTIEGKSTCA 59
 DB 2 KDRPDPCELPADTGPCRVPRPSFYNNDEKCKLEFIYGGCGGANNFRTIEGKSTCS 60
 RESULT 8
 ID AAY15139 standard; Protein; 59 AA.
 AC AAY15139;
 XX 07-FEB-2000 (first entry)
 DE Txln 2 Plasmin inhibitor protein.
 XX
 XX Textillin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; control;
 KM haematopoietic; cytosolic activity; homology; specificity; Aprotinin;
 KM Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 XX W09958569-A1.
 PD 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI/) LAVIN M F J.
 PA (GAFF/) GAFFNEY P J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ29018.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX
 PS Claim 8b; Page 69; 112pp; English.

XX
 CC The present sequence is the Textillin protein, Txln 2 that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln 2 has 413 and
 CC 55% homology with Aprotinin and Taicotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 CC
 SQ Sequence 59 AA;
 Query Match 63.5%; Score 217; DB 21; Length 59;
 Best Local Similarity 64.4%; Pred. No. 1.1e-19; Mismatches 15; Indels 0; Gaps 0;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 OY 1 KDHPKFCLELPATGSCGNVPRFYNNADHHQCLKFIYGGCGGANNFRTIEGKSTCA 59
 DB 1 KDRPDPCELPADTGPCRVPRPSFYNNDEKCKLEFIYGGCGGANNFRTIEGKSTCA 59
 RESULT 9
 ID AAY15146 standard; Protein; 63 AA.
 AC AAY15146;
 XX 07-FEB-2000 (first entry)
 DE Proform of Txln 2 protein.
 XX
 XX Textillin proform; Txln 2; plasmin inhibitor; single stage inhibitor;
 KM Australian brown snake; conserved cysteine residue; stability; Aprotinin;
 KM haematopoietic; cytosolic activity; homology; specificity; control;
 KM Taicotoxin-associated plasmin inhibitor; TAC; inhibitory efficiency;
 KM fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KM fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KM reduced propensity; thrombosis.
 XX
 OS Pseudonaja textilis textilis.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Leader peptide
 FT 25..83
 FT /label= Txln-2 protein
 FT /note= "Textillin-2"
 XX
 XX W09958569-A1.
 PD 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-AU00343.
 XX
 XX 11-MAY-1998; 98AU-0003450.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASI P P.
 PA (LAVI/) LAVIN M F J.
 PA (GAFF/) GAFFNEY P J.
 XX
 PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filipovich IV;
 XX WPI; 2000-039073/03.
 DR N-PSDB; AAZ29025.
 XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX

PT agents -
 XX Claim 40b; Page 71; 112pp; English.
 CC The present sequence is the proform of the Textillinin protein, Txln 2,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln 2 has 43% and
 CC 55% homology with Aprotinin and Talcotoxin-associated plasmin inhibitor
 CC (TAC), respectively. Txln has high specificity for plasmin and low
 CC inhibitory efficiency, that can transiently affect the delicate balance
 CC between enzymes and inhibitors of the fibrinolytic system, controlling
 CC the fluidity of blood. The plasmin inhibitors are useful for alleviating
 CC blood loss, following major surgery or trauma. Conjugates of the plasmin
 CC inhibitor and an anti-fibrin antibody are useful as anti-tumour agents.
 CC They have reduced propensity to cause thrombosis.
 SQ Sequence 83 AA;
 Query Match 63.5%; Score 217; DB 21; Length 83;
 Best Local Similarity 64.4%; Pred. No. 1.5e-19;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 QY 1 KDHPKCELPARTGCKGNVPRFYNNADHROCKLRTYGGCGGNANFKTIEEGKSTCA 59
 DB 25 KDRPELCLEPPTGPCRVAPSPFYNNPDCKLEFIYGGCGGNANFKTIEEGKSTCA 83
 RESULT 10
 AAR9146 AAR9146 standard; protein; 58 AA.
 AC AAR9146;
 DT 12-FEB-1997 (first entry)
 DE Aprotinin-like Kunitz domain.
 KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.
 OS Synthetic.
 PN MO9620278-A2.
 PD 04-JUL-1996.
 PF 15-DEC-1995; 95WO-US16349.
 PR 16-DEC-1994; 94US-0358160.
 PA (PROT-) PROTEIN ENG CORP.
 PI Guerman SK, Kent RB, Ladner RC, Ley AC, Markland W;
 PI Roberts BL;
 DR WPI; 1996-321851/32.
 PT New engineered inhibitors of human neutrophil elastase - contd.
 PT aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or
 PT other respiratory disorders
 PS Example 23; Page 47; 105pp; English.
 CC Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the
 CC elimination of pathogens and the restructuring of connective tissue.
 CC In cases of reduction of the circulating alpha-1-protease inhibitor
 CC (API or alpha antitrypsin), or the inactivation of API by oxidation
 CC (smokers emphysema), extensive destruction of the lung tissue may

CC result from uncontrolled elastolytic activity of human neutrophil
 CC elastase. Other respiratory disorders such as cystic fibrosis are
 CC thought to be caused by human neutrophil elastase release by
 CC neutrophils. The genetically engineered human derived Kunitz
 CC domains can be used to treat such respiratory disorders. See
 CC AAR9146-R99211.
 SQ Sequence 58 AA;
 Query Match 61.7%; Score 211; DB 17; Length 58;
 Best Local Similarity 68.5%; Pred. No. 5.8e-19;
 Matches 37; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 QY 4 PRCELPARTGCKGNVPRFYNNADHROCKLRTYGGCGGNANFKTIEEGKSTC 57
 DB 2 PFCLELPARTGCRAMIRPRFYNNASGCKEPIYGGCGGNANFKTIEEGKSTC 55
 RESULT 11
 AAY15142
 ID AAY15142 standard; protein; 59 AA.
 AC AAY15142;
 DT 07-FEB-2000 (first entry)
 DE Txln 5 Plasmin inhibitor protein.
 KW Textillinin protein; Txln 5; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytostatic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.
 OS Pseudonaja textilis textilis.
 PN WO958569-A1.
 PD 18-NOV-1999.
 PF 07-MAY-1999; 99WO-AU00343.
 PR 11-MAY-1998; 98AU-0003450.
 PA (UYOU) UNIV QUEENSLAND.
 PA (NABT-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P F.
 PA (LAVI/) LAVIN M F.
 PA (GAFF/) GAFFNEY P J.
 PI Masci PP, Lavlin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 DR WPI; 2000-039073/03.
 DR N-PSDB; AA229021.
 PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 PS Claim 8e; Page 69; 112pp; English.
 CC The present sequence is the Textillinin protein, Txln 5, that is a
 CC single stage competitive inhibitor of plasmin. It is isolated from the
 CC Australian brown snake, Pseudonaja textilis textilis. It has six
 CC conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytostatic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced
 CC propensity to cause thrombosis.

XX SQ Sequence 59 AA;

Query Match 58.8%; Score 201; DB 21; Length 59;
 Best Local Similarity 61.0%; Pred. No. 1.1e-17;
 Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANNFRTIEBKGSTCA 59
 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANNFRTIEBKGSTCA 59

Db 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANNFRTIEBKGSTCA 59

RESULT 12
 AAY15149
 ID AAY15149 standard; Protein; 83 AA.

XX AC AAY15149;
 XX DT 07-FEB-2000 (first entry)
 XX DE Proform of Txln 5 protein.

XX KW Textillinin proform; Txln 5; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytosolic activity; specificity; inhibitory efficiency;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma; enzyme;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW reduced propensity; thrombosis.

XX OS Pseudonaja textilis textilis.

XX FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Leader_peptide
 FT /label= Txln-5 protein
 FT /note= "Textillinin-5"

XX PN WO9958569-A1.
 XX PD 18-NOV-1999.
 XX PF 07-MAY-1999; 99WO-AU00343.
 XX PR 11-MAY-1998; 98AU-0003450.

XX PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFN/) GAFNEY P J.

XX PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 DR WPI: 2000-039073/03.
 DR N-PSDB; AAZ29028.

XX PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX PS Claim 40e; Page 72; 112pp; English.

XX CC The present sequence is the proform of the Textillinin protein, Txln 5,
 CC that is a single stage competitive inhibitor of plasmin. It is isolated
 CC from the Australian brown snake, Pseudonaja textilis textilis. It has
 CC six conserved cysteine residues, that endow them great stability. This
 CC sequence has haematopoietic and cytosolic activity. Txln has high
 CC specificity for plasmin and low inhibitory efficiency, that can
 CC transiently affect the delicate balance between enzymes and inhibitors
 CC of the fibrinolytic system, controlling the fluidity of blood. The
 CC plasmin inhibitors are useful for alleviating blood loss, following
 CC major surgery or trauma. Conjugates of the plasmin inhibitor and an
 CC anti-fibrin antibody are useful as anti-tumour agents. They have reduced

CC propensity to cause thrombosis.

XX SQ Sequence 83 AA;

Query Match 58.8%; Score 201; DB 21; Length 83;
 Best Local Similarity 61.0%; Pred. No. 1.6e-17;
 Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANNFRTIEBKGSTCA 59
 1 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANNFRTIEBKGSTCA 59

Db 25 KDHPKCELPATGSCCKGNVPRFYNNADHQCCKFYGGCGGNANNFRTIEBKGSTCA 83

RESULT 13
 AAY15154
 ID AAY15154 standard; Protein; 60 AA.

XX AC AAY15154;
 XX DT 07-FEB-2000 (first entry)
 XX DE Plasmin inhibitor Txln 2, encoded by partial cDNA sequence.

XX KW Textillinin protein; Txln 2; plasmin inhibitor; single stage inhibitor;
 KW Australian brown snake; conserved cysteine residue; stability; control;
 KW haematopoietic; cytosolic activity; homology; enzyme;
 KW fluidity of blood; alleviate; blood loss; major surgery; trauma;
 KW fibrinolytic system; conjugate; anti-fibrin antibody; anti-tumour agent;
 KW inhibitory efficiency; reduced propensity; thrombosis.

XX OS Pseudonaja textilis textilis.

XX FH Key Location/Qualifiers
 FT Misc-difference 24 /note= "encoded by TTG"
 FT Misc-difference 45 /note= "encoded by GAT"
 FT Misc-difference 49 /note= "encoded by ATG"
 FT Misc-difference 59 /note= "encoded by CCN"

XX PN WO9958569-A1.
 XX PD 18-NOV-1999.
 XX PF 07-MAY-1999; 99WO-AU00343.
 XX PR 11-MAY-1998; 98AU-0003450.

XX PA (UYOU) UNIV QUEENSLAND.
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
 PA (MASC/) MASC P P.
 PA (LAVI/) LAVIN M F.
 PA (GAFN/) GAFNEY P J.

XX PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
 DR WPI: 2000-039073/03.
 DR N-PSDB; AAZ29048.

XX PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
 PT agents -
 XX PS Disclosure; Fig 7; 112pp; English.

XX CC The present amino acid sequence is the Txln 2, Textillinin protein
 CC encoded by the partial cDNA sequence. It is a single stage competitive
 CC inhibitor of plasmin. It is isolated from the Australian brown snake,
 CC Pseudonaja textilis textilis. Txln has high specificity for plasmin and
 CC low inhibitory efficiency that can transiently affect the delicate
 CC balance between enzymes and inhibitors of the fibrinolytic system,
 CC controlling the fluidity of blood. The plasmin inhibitors are useful for

Query Match 56.1%; Score 192; DB 21; Length 83;
 Best Local Similarity 57.6%; Pred. No. 2.1e-16;
 Matches 34; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
 Qy 1 KDHPRFCELPAPETGSCGNVPRFYTNADHOCLEFIYGGCGGNANPKTIERGKSTCA 59
 Db 25 KDRPFCELPADIGFWDDFTGAFHYSPREHECIEFIYGGCKGNANFNTOECSTCA 83

Search completed: January 23, 2004, 10:24:35
 Job time : 28.4613 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:23 ; Search time 9.14085 Seconds
(without alignments)
620.725 Million cell updates/sec

Title: US-09-700-179A-2.

Sequence: 1 KDRDPFCHLPADTGPCRVRF.....CEGNANPFITKECESTCA 59

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	63.6	62	2	A4180
2	214	62.8	65	1	TIIVIC
3	204	59.8	62	2	S07451
4	201	58.9	57	1	TINJVC
5	201	58.9	61	1	TIIVIT1
6	198	58.1	57	1	TIIVIT2
7	195	57.2	62	2	S19327
8	194	56.9	57	2	S13846
9	189	55.4	110	1	TIIVOR
10	188	55.1	58	1	TIHABK
11	179	52.5	57	2	B59399
12	179	52.5	59	1	TIIVED
13	179	52.5	59	2	A53399
14	178	52.2	60	1	TIIVR2
15	169	49.6	57	1	TIIVPA
16	169	49.6	302	1	TIIVTK
17	169	49.6	396	2	S53325
18	168	49.3	79	1	TIIVPV
19	168	49.3	304	1	UC2264
20	167	49.0	57	2	A59204
21	165	48.4	57	2	TIIVBP
22	165	48.4	235	2	A54951
23	165	48.4	299	2	I46937
24	165	48.4	300	2	S12143
25	163	47.8	252	2	UG0185
26	161	47.2	304	2	TIIVGK
27	160	46.9	3176	1	CGH03A
28	158	46.3	59	2	S00371
29	156	45.7	58	2	S10063

ALIGNMENTS

30	156	45.7	100	1	TIIVOR	basic proteinase i
31	155	45.5	122	1	A55115	uterine plasmin/tr
32	154	45.2	100	1	TIIVOSP	spleen basic prote
33	154	45.2	747	2	JH0773	Alzheimer's diseas
34	153	44.9	57	1	TIIVPV	venom basic protei
35	152	44.6	60	1	TIIVOR	serum basic protei
36	152	44.6	76	2	S04855	Alzheimer's diseas
37	152	44.6	100	2	A32282	Alzheimer's diseas
38	150	44.0	76	2	S03607	Alzheimer's diseas
39	150	44.0	76	2	S06678	Alzheimer's diseas
40	150	44.0	111	2	S41082	amyloid precursor
41	150	44.0	484	4	A32761	hypothetical Alzhe
42	150	44.0	770	1	ORH044	Alzheimer's diseas
43	150	44.0	2225	2	T26063	hypothetical prote
44	149	43.7	55	2	S30332	proteinase inhibit
45	149	43.7	751	2	A49974	beta-amyloid precu

RESULT 1

A4180
calicotoxin serine proteinase inhibitor component - Australian taipan
C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #ext_change 07-Feb-1997
C:Accession: A4180
R:Posami, L.D.; Martin, B.M.; Yatani, A.; Mochizuki-Morales, J.; Zamudio, F.Z.; Gurrola, T.; Toxicon 30, 1343-1364, 1992
A>Title: Isolation and physiological characterization of calicotoxin, a complex toxin w:
A:Reference number: A4180; PMID:93134601; PMID:1485334
A:Accession: A4180
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Experimental source: subsp. scutellatus, venom
A>Note: sequence extracted from NCBI backbone (NCBI:122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
C:Keywords: serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
Best Local Similarity 63.6%; Score 217; DB 2; Length 62;
Matches 36; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 KDRDPFCHLPADTGPCRVRFPSFYNNPDEKCLIFYYGCEGNANPFITKECESTC 57
DB 1 KDRPFCHLPADTGPCRVRFPSFYNNPDEKCLIFYYGCEGNANPFITKECESTC 57

RESULT 2

TIIVIC
venom basic proteinase inhibitor III - sand viper
N:Alternate names: venom chymotrypsin inhibitor
C:Species: Viper a ammodytes (sand viper)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #ext_change 16-Aug-1996
C:Accession: A01223
R:Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A>Title: The primary structure Of Viper a ammodytes venom chymotrypsin inhibitor.
A:Reference number: A01223
A:Accession: A01223
A:Molecule type: protein
A:Residues: 1-65 <NT>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom
C:Keywords: serine proteinase inhibitor; venom
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:7-57,16-40,32-53/Diulfide bonds: #status predicted
F:17/inhibitory site: Denu (chymotrypsin) #status predicted

Query Match
Best Local Similarity 62.8%; Score 214; DB 1; Length 65;
Matches 37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KDRPDCSLPADTGPCRVPRPSPFYNNPDEKCLERFYGGCGGNANNFITKECESTCA 59
 Db 1 RDRPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTCA 59

RESULT 3

S07451
 A:Accession: S07451
 A:Reference number: S07451
 A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia
 A:Keywords: serine proteinase inhibitor
 A:Residues: 1-59 <WUN>
 A:Molecule type: protein
 C:Species: Anemonia sulcata (snake-locks sea anemone)
 C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C:Accession: S07451; B27222
 R:Munderer, G.; Machleidt, W.; Fritz, H.
 Meth. Enzymol. 80, 816-820, 1981
 A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia
 A:Reference number: S07451
 A:Accession: S07451

Query Match 59.8%; Score 204; DB 1; Length 62;
 Best Local Similarity 66.7%; Pred. No. 2.7e-16;
 Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
 A:Residues: 1-59 <WUN>
 A:Molecule type: protein
 C:Species: Anemonia sulcata (snake-locks sea anemone)
 C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C:Accession: S07451; B27222
 R:Munderer, G.; Machleidt, W.; Fritz, H.
 Meth. Enzymol. 80, 816-820, 1981
 A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia
 A:Reference number: S07451
 A:Accession: S07451

Query Match 59.8%; Score 204; DB 2; Length 62;
 Best Local Similarity 66.7%; Pred. No. 2.7e-16;
 Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
 A:Residues: 1-59 <WUN>
 A:Molecule type: protein
 C:Species: Anemonia sulcata (snake-locks sea anemone)
 C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C:Accession: S07451; B27222
 R:Munderer, G.; Machleidt, W.; Fritz, H.
 Meth. Enzymol. 80, 816-820, 1981
 A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia
 A:Reference number: S07451
 A:Accession: S07451

Qy 7 CELPADTGPCRVPRPSPFYNNPDEKCLERFYGGCGGNANNFITKECESTC 57
 Db 5 CELPKVVGCPARPRPSPFYNNSSSKCEKFIYGGCGGNANNFITKECESTC 55

RESULT 4

Qy 7 CELPADTGPCRVPRPSPFYNNPDEKCLERFYGGCGGNANNFITKECESTC 57
 Db 5 CELPKVVGCPARPRPSPFYNNSSSKCEKFIYGGCGGNANNFITKECESTC 55
 A:Residues: 1-57 <HOK>
 A:Molecule type: protein
 C:Species: Naja naja (Cape cobra)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01217
 R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
 o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01217

Query Match 58.9%; Score 201; DB 1; Length 57;
 Best Local Similarity 63.6%; Pred. No. 5.4e-16;
 Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
 A:Residues: 1-57 <HOK>
 A:Molecule type: protein
 C:Species: Naja naja (Cape cobra)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01217
 R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
 o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01217

Qy 3 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 57
 Db 1 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 55

RESULT 5

Qy 3 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 57
 Db 1 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 55
 A:Residues: 1-62 <SID>
 A:Molecule type: protein
 C:Species: Eristocophis maculatus (leaf-nosed viper)
 C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S19327
 R:Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
 FEBS Lett. 294, 141-143, 1991
 A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Lea
 A:Reference number: S19327; MUID:92077130; PMID:1743283
 A:Accession: S19327

C:Species: Viper a ammodytes ammodytes (western sand viper)
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996
 C:Accession: A01222

Query Match 58.9%; Score 201; DB 1; Length 61;
 Best Local Similarity 57.6%; Pred. No. 5.8e-16;
 Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
 A:Residues: 1-61 <RT>
 A:Molecule type: protein
 C:Species: Viper a ammodytes ammodytes (western sand viper)
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996
 C:Accession: A01222
 R:Rittonja, A.; Meloni, B.; Gubensek, F.
 Blochm. Biophys. Acta 748, 429-435, 1983
 A:Title: The primary structure of Viper a ammodytes venom trypsin inhibitor I.
 A:Reference number: A01222; MUID:84053385; PMID:6639951
 A:Accession: A01222

Query Match 58.9%; Score 201; DB 1; Length 61;
 Best Local Similarity 57.6%; Pred. No. 5.8e-16;
 Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
 A:Residues: 1-61 <RT>
 A:Molecule type: protein
 C:Species: Viper a ammodytes ammodytes (western sand viper)
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Aug-1996
 C:Accession: A01222
 R:Rittonja, A.; Meloni, B.; Gubensek, F.
 Blochm. Biophys. Acta 748, 429-435, 1983
 A:Title: The primary structure of Viper a ammodytes venom trypsin inhibitor I.
 A:Reference number: A01222; MUID:84053385; PMID:6639951
 A:Accession: A01222

Qy 1 KDRPDCSLPADTGPCRVPRPSPFYNNPDEKCLERFYGGCGGNANNFITKECESTCA 59
 Db 1 ODHPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTCA 59

RESULT 6

Qy 1 KDRPDCSLPADTGPCRVPRPSPFYNNPDEKCLERFYGGCGGNANNFITKECESTCA 59
 Db 1 ODHPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTCA 59
 A:Residues: 1-57 <HOK>
 A:Molecule type: protein
 C:Species: Naja naja (Cape cobra)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01216
 R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
 o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01216

Query Match 58.1%; Score 198; DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 1.2e-15;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 A:Residues: 1-57 <HOK>
 A:Molecule type: protein
 C:Species: Naja naja (Cape cobra)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01216
 R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
 o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01216

Qy 3 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 57
 Db 1 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 55

RESULT 7

Qy 3 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 57
 Db 1 RDPFCFLPATGTGCKARIRSFHNRAAQCLERFYGGCGGNANNFITKECESTC 55
 A:Residues: 1-62 <SID>
 A:Molecule type: protein
 C:Species: Eristocophis maculatus (leaf-nosed viper)
 C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S19327
 R:Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
 FEBS Lett. 294, 141-143, 1991
 A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Lea
 A:Reference number: S19327; MUID:92077130; PMID:1743283
 A:Accession: S19327

F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 57.2%; Score 195; DB 2; Length 62;
Best Local Similarity 61.1%; Pred. No. 2.8e-15;
Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 6 FCELPADTGPCRVPRFPSPFYNNPDEKCLFEIYGCGEGNANFTTKECESTCA 59
Db 1 FCVLPDPGVCKAHIPRYNNPASKCKKRFIYGCGEGNANFTTKECHTCA 54

RESULT 8

venom animal Kunitz-type trypsin inhibitor - Indian cobra

C/Species: Naja naja naja (Indian cobra)

C/Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #ext_change 17-Mar-2000

C/Accession: S13846

R/Shafiq, J.; Beg, O.U.; Yin, S.J.; Zaidi, Z.H.; Joernvall, H.

Eur. J. Biochem. 194, 337-341, 1990

A/Title: Primary structure and functional properties of cobra (Naja naja naja) venom Kunitz-type proteinase inhibitor

A/Accession: S13846; MUID:9109304; PMID:1702708

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <SHA>

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 56.9%; Score 194; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 3.3e-15;
Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 3 RPDPELPADTGPCRVPRFPSPFYNNPDEKCLFEIYGCGEGNANFTTKECESTC 57
Db 1 RPFCELPAPAKGLCKAHKPAFYNNKDSHRCQKFIYGCAGANRFTIDECHNRTC 55

RESULT 9

TITTROR

basic proteinase inhibitor - loggerhead

C/Species: Caretta caretta (loggerhead)

C/Date: 31-May-1979 #sequence_revision 23-Oct-1981 #ext_change 05-Aug-1994

C/Accession: A01224

R/Kato, I.; Tomimaga, N.

Fed. Proc. 38, 832, 1979

A/Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A/Reference number: A01224

A/Accession: A01224

A/Molecule type: protein

A/Residues: 1-110 <KAT>

C/Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C/Suprafamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh

C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8-58,17-41,33-54,67-93,76-97,80-92,86-101/Disulfide bonds: #status predicted

F;18/inhibitory site: Lys (trypsin) #status predicted

Query Match 55.4%; Score 189; DB 1; Length 110;
Best Local Similarity 53.6%; Pred. No. 2.4e-14;
Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 2 DRDPCELPADTGPCRVPRFPSPFYNNPDEKCLFEIYGCGEGNANFTTKECESTC 57
Db 3 DRKDILRLPPEQPCCKGRIPRYNNPASKCKKRFIYGCGEGNANFTTKECESTC 58

RESULT 10

TITABK

isoinhibitor K (BPI type) - Roman snail

C/Species: Helix pomatia (Roman snail)

C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #ext_change 05-Aug-1994

C/Accession: A91232; A01225

R/Teschke, H.; Dietl, T.

Eur. J. Biochem. 58, 439-451, 1975

A/Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequ

A/Reference number: A91232; MUID:76043680; PMID:1183446

A/Accession: A91232

A/Molecule type: protein

A/Residues: 1-58 <TSC>

R/Dietl, T.; Teschke, H.

Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976

A/Title: Die Disulfidbrücke des Trypsin-Kalikrein-Inhibitors K aus Weinbergsschnecke

A/Reference number: A91666; MUID:76141310; PMID:3462

A/Content: annotation; disulfide bonds

C/Comment: This is one of several isoinhibitors of broad specificity that are secreted

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C/Keywords: pyroglutamic acid; serine proteinase inhibitor

F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 55.1%; Score 188; DB 1; Length 58;
Best Local Similarity 52.7%; Pred. No. 1.6e-14;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 3 RPDPELPADTGPCRVPRFPSPFYNNPDEKCLFEIYGCGEGNANFTTKECESTC 57
Db 3 RPFCELPAPAKGLCKAHKPAFYNNKDSHRCQKFIYGCAGANRFTIDECHNRTC 57

RESULT 11

short epelion-dendrotoxin His55, subunit - Dendroaspis angusticeps

C/Species: Dendroaspis angusticeps

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #ext_change 17-May-2002

C/Accession: B59399

R/Signle, R.; Hackett, M.; Aird, S.D.

Toxicol. 40, 297-308, 2002

A/Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis

A/Reference number: A59399

A/Accession: B59399

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-57 <AIR>

C/Suprafamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

F;5-55/Disulfide bonds: #status experimental

F;14-38/Disulfide bonds: #status experimental

F;30-51/Disulfide bonds: #status experimental

Query Match 52.5%; Score 179; DB 2; Length 57;
Best Local Similarity 57.7%; Pred. No. 1.7e-13;
Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 6 FCELPADTGPCRVPRFPSPFYNNPDEKCLFEIYGCGEGNANFTTKECESTC 57
Db 4 FCELPADTGPCRVPRFPSPFYNNPDEKCLFEIYGCGEGNANFTTKECHNRTC 55

RESULT 12

TITBED

venom basic proteinase inhibitor B - black mamba

C/Species: Dendroaspis polylepsis polylepsis (black mamba)

C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #ext_change 16-Aug-1996

C/Accession: A01215

R/Joubert, F.J.; Strydom, D.J.

Eur. J. Biochem. 87, 191-198, 1978

A/Title: Snake venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis p

A/Reference number: A01215; MUID:78214615; PMID:666688

A/Accession: A01215

A/Molecule type: protein

A/Residues: 1-59 <JOU>

A/Note: this protein inhibits trypsin and binds transition metal ions such as copper a

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C/Keywords: serine proteinase inhibitor; venom
 F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F/7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 52.5%; Score 179; DB 1; Length 59;
 Best Local Similarity 57.7%; Pred. No. 1,7e-13;
 Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 6 FCELPADTGPCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKCESTC 57
 DB 6 FCKLPAPGPCAKSIAPFYNNMAKKCQLPHYGGCGGNANRFTIECRAC 57

RESULT 13

Long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps

C/Species: Dendroaspis angusticeps
 C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002

C/Accession: A59399

R/Sigle, R.; Hackert, M.; Aird, S.D.
 Toxicon 40, 297-308, 2002.

A/Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis
 A/Reference number: A59399

A/Accession: A59399

A/Status: preliminary

A/Molecule type: protein

A/Residues: 159 <AIR>

A/Note: trypsin inhibitor; K+ channel antagonist

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

F/7-57/Disulfide bonds: #status experimental

F/16-40/Disulfide bonds: #status experimental

F/32-53/Disulfide bonds: #status experimental

Query Match 52.5%; Score 179; DB 2; Length 59;
 Best Local Similarity 57.7%; Pred. No. 1,7e-13;
 Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 6 FCELPADTGPCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKCESTC 57
 DB 6 FCKLPAPGPCAKSIAPFYNNMAKKCQLPHYGGCGGNANRFTIECRAC 57

RESULT 14

TIVRV2

venom basic proteinase inhibitor II - Russell's viper

C/Species: Viperia russelli (Russell's viper)
 C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C/Accession: A01221

R/Takahashi, H.; Iwanaga, S.; Kitagawa, T.; Hokama, Y.; Suzuki, T.
 J. Biochem. 76, 723-733, 1974

A/Title: Snake venom proteinase inhibitors. II. Chemical structure of inhibitor II isolat

A/Reference number: A01221; PMID:75060360; PMID:4436285

A/Accession: A01221

A/Molecule type: protein

A/Residues: 1-60 <TRX>

C/Comment: This inhibitor has activity similar to that of bovine basic protease inhibit

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C/Keywords: serine proteinase inhibitor; venom

F/7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/7-57,16-40,32-53/Disulfide bonds: #status experimental

Query Match 52.2%; Score 178; DB 1; Length 60;
 Best Local Similarity 53.6%; Pred. No. 2,3e-13;
 Matches 30; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 DRPFCFLPADTGPCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKCESTC 57
 DB 2 DRPFCFLPADTGPCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKCESTC 57

RESULT 15

TIEPVA

venom basic proteinase inhibitor K - eastern green mamba
 N/Alternate names: dendrotoxin delta-DarX
 C/Species: Dendroaspis angusticeps (eastern green mamba)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
 C/Accession: A91691; C32508; A01213
 R/Joubert, F.J.; Taljaard, N.
 Hoppe-Seyler's Z. Physiol. Chem. 361, 661-674, 1980
 A/Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroas
 A/Reference number: A91691; PMID:81045446; PMID:7429422
 A/Accession: A91691

A/Molecule type: protein

A/Residues: 1-57 <QOU>

R/Benshin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaubein, M.P.
 Mol. Pharmacol. 34, 152-159, 1988

A/Title: Four polypeptide components of green mamba venom selectively block certain po

A/Reference number: A93137; PMID:88318591; PMID:2457792

A/Accession: C32508

A/Molecule type: protein

A/Residues: 1-21 <BEN>

A/Note: the amino acid composition of the inhibitor is identical with that predicted f

C/Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological

C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor hom

C/Keywords: venom

F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F/5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 49.6%; Score 169; DB 1; Length 57;
 Best Local Similarity 55.8%; Pred. No. 2,2e-12;
 Matches 29; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 6 FCELPADTGPCRVRFPSPFYNNPDEKCKLEFIYGGCGGNANFTTKCESTC 57
 DB 4 YCKLPVRYGPKCKKIPSPFYNNMAKKCQLPFYGGCGGNANRFTIECRAC 55

Search completed: January 23, 2004, 10:28:10
 Job time: 10.1408 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:17:42 ; Search time 5.40141 Seconds

(without alignments)
513.676 Million cell updates/sec

Title: US-09-700-179a-2

Sequence: 1 KDRPFCCLPADTGCRVRF.....CEGNANNFTKECESTCA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	62.8	65	1	IVB3_VIPAA
2	204	59.8	62	1	IP52_ANESU
3	201	58.9	57	1	IVB2_NAJNI
4	201	58.9	61	1	IVB1_VIPAA
5	198	58.1	57	1	IVB2_HEMHA
6	195	57.2	62	1	IVB2_ERIMA
7	194	56.9	57	1	IVB2_NAJNI
8	192	56.3	65	1	IVB1_BUNFA
9	189	55.4	110	1	IBP_CARCR
10	188	55.1	58	1	ISIK_HELPO
11	187.5	55.0	55	1	CSTI_BOMMO
12	179	52.5	58	1	AXPI_ANTAF
13	179	52.5	59	1	IVB2_DENPO
14	179	52.5	230	1	TFP2_MOUSE
15	178	52.2	60	1	IVB2_DABRU
16	169	49.6	57	1	IVB2_DEMAN
17	169	49.6	302	1	TFP1_RAT
18	169	49.6	306	1	TFP1_MOUSE
19	168	49.3	57	1	IVB2_DENPO
20	168	49.3	58	1	IVB2_OPBHA
21	168	49.3	304	1	TFP1_NACMU
22	167	49.0	58	1	AXPI_ANTAF
23	165	48.4	57	1	SBP1_SABBU
24	165	48.4	235	1	TFP2_HUMAN
25	165	48.4	300	1	TFP1_RABIT
26	163	47.8	252	1	SPT2_MOUSE
27	162.5	47.7	69	1	CRPT_BOOMI
28	161	47.2	252	1	SPT2_HUMAN
29	161	47.2	304	1	TFP1_HUMAN
30	160	46.9	133	1	EPTI_HUMAN
31	160	46.9	3176	1	CAB3_HUMAN
32	156	45.7	100	1	BPT1_BOVIN
33	156	45.7	513	1	SPT1_HUMAN

34	155	45.5	122	1	UPT1_PIG	Q29100 sus scrofa
35	154	45.2	100	1	BPT2_BOVIN	P04815 bos taurus
36	153	44.9	57	1	IVB2_DENPO	P00983 dendroaspis
37	152	44.6	60	1	IBP3_BOVIN	P00975 bos taurus
38	152	44.6	770	1	A4_MOUSE	P12023 m amyloid b
39	150	44.0	76	1	A4_MACMU	P29216 macaca mula
40	150	44.0	751	1	A4_SAIIC	Q95241 s amyloid b
41	150	44.0	770	1	A4_HUMAN	P05067 h amyloid b
42	150	44.0	770	1	A4_MACFA	P53601 m amyloid b
43	150	44.0	770	1	A4_PIG	P79307 r amyloid b
44	150	44.0	770	1	A4_RAT	P08592 r amyloid b
45	149	43.7	55	1	ISH1_STOHE	P31713 scolichactis

ALIGNMENTS

RESULT 1	IVB3_VIPAA	STANDARD;	PRT;	65 AA.
ID	IP52_ANESU			
AC	P00932;			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	21-JUL-1986 (Rel. 01, Last annotation update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Venom basic protease inhibitor III (Venom chymotrypsin inhibitor).			
OS	Vipera ammodytes ammodytes (Western sand viper).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;			
OC	Viperidae; Viperinae; Vipera.			
OX	NCBI_TaxID=8705;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RA	Ritonja A., Meloun B., Gubensek F.;			
RT	"The primary structure of Vipera ammodytes venom chymotrypsin inhibitor."			
RL	Biochim. Biophys. Acta 746:138-145(1983).			
CC	-1- FUNCTION: This protein inhibits chymotrypsin.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	PIR; A01223; TIVTC.			
DR	HSSP; P31713; ISHP.			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF00014; Kunitz_BPTI; 1.			
DR	Prodom; PD000222; Kunitz_BPTI; 1.			
DR	SMART; SM00131; KUI; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Serine protease inhibitor.			
FT	DISULFID 7 57			
FT	DISULFID 16 40			
FT	DISULFID 32 53			
FT	ACT SITE 17 18			
FT	SEQUENCE 65 AA; 7556 MW; 9D526F8E3BF7CC57 CRC64;			
REACTIVE BOND (BY SIMILARITY).				
Query Match	62.8%; Score 214; DB 1; Length 65;			
Best Local Similarity	62.7%; Pred. No. 3.2e-19;			
Matches	37; Conservative 3; Mismatches 19; Indels 0; Gaps 0;			
Qy	1 KDRPFCCLPADTGCRVRFPSFYNPDEKCLFTYGGCEGNANNFTKECESTCA 59			
Db	1 RDRPKCYLPADRGRCIAVMPFRYYPASVKCKFTYGGCEGNANNFTKECESTCA 59			
RESULT 2	IP52_ANESU	STANDARD;	PRT;	62 AA.
ID	IP52_ANESU			
AC	P10280;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Protease inhibitor 5 II (SAS II).			
OS	Anemonia sulcata (Snake-locks sea anemone).			

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OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
CC Nymathea; Actinidae; Anemona.
OX NCBI_Taxid=6108;
RN [1]
RP SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
RT Anemona sulcata."
RL Meth. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide
RT from the sea anemone Metridium senile."
RL Naturwissenschaften 74:395-396(1987).
CC -1- FUNCTION: INHIBITOR OF KALIKREINS.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P31713; 1SHP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 13 13 P -> R.
FT VARIANT 16 16 R -> G.
FT VARIANT 17 17 R -> G.
FT VARIANT 25 25 S -> L.
FT VARIANT 28 28 K -> R.
FT VARIANT 39 39 G -> R.
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 59.8%; Score 204; DB 1; Length 62;
Best Local Similarity 66.7%; Pred. No. 4.8e-18;
Matches 34; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 7 CELPADGPRCPVRPSPFYNNDEKKCLEFYTGCGEGNANNFTKECESTC 57
DB 5 CELPKVGPCKARFPRTYNNSSKRCERFYTGCGEGNANNFTKECEKVC 55

RESULT 3
ID IVB2_NAJNI STANDARD; PRT; 57 AA.
AC P00986;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 01, Last annotation update)
DE Venom basic protease inhibitor II.
OS Naja naja (Cape cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Naja.
OX NCBI_Taxid=6655;
RN [1]
RP SEQUENCE.
RA TISSUE=Venom;
RX MEDLINE=76237547; PubMed=950337;
RA Hokama Y., Iwanaga S., Tateuchi T., Suzuki T.;
RT "Snake venom proteinase inhibitors. III. Isolation of five
RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
RT (Ringal's cobra) and Naja naja (Cape cobra) and the complete amino
RT acid sequences of two of them."
RL J. Biochem. 79:559-578(1976).
CC -1- FUNCTION: The activity of this inhibitor is probably similar to
CC that of bovine basic protease inhibitor.
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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01217; TINVJC.
DR HSSP; P00981; IDPK.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

Query Match 58.9%; Score 201; DB 1; Length 57;
Best Local Similarity 63.6%; Pred. No. 1e-17;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 3 RPDCELPADGPRCPVRPSPFYNNDEKKCLEFYTGCGEGNANNFTKECESTC 57
DB 1 RPRCELPADGPRCPVRPSPFYNNDEKKCLEFYTGCGEGNANNFTKECESTC 55

RESULT 4
ID IVB1_VIPAA STANDARD; PRT; 61 AA.
AC P00991;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 01, Last annotation update)
DE Venom basic protease inhibitor I (Venom trypsin inhibitor I).
OS Vipera ammodytes ammodytes (Western sand viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Vipera.
OX NCBI_Taxid=8705;
RN [1]
RP SEQUENCE.
RA TISSUE=Venom;
RX MEDLINE=84053385; PubMed=6639951;
RA Riconia A., Meloun B., Gubensek F.;
RT "The primary structure of Vipera ammodytes venom trypsin inhibitor
RT I."
RL Biochim. Biophys. Acta 748:429-435(1983).
CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01222; TIVT1.
DR HSSP; P31713; 1SHP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
SQ SEQUENCE 61 AA; 6865 MW; FC8285F579FE3795 CRC64;

Query Match 58.9%; Score 201; DB 1; Length 61;
Best Local Similarity 57.6%; Pred. No. 1.1e-17;
Matches 34; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 KDPDCELPADGPRCPVRPSPFYNNDEKKCLEFYTGCGEGNANNFTKECESTC 59
DB 1 QDHPCELPADGPRCPVRPSPFYNNDEKKCLEFYTGCGEGNANNFTKECESTC 59
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RESULT 5
 IVD2_HEMMA STANDARD; PRT; 57 AA.
 AC P00981;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Hemachatus haemachatus (Ringhals) (Sapedon haemachatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Hemachatus.
 OC NCBI_TaxID=8626;
 RX MEDLINE=76237547; PubMed=950337;
 RA Hokama Y., Iwanaga S., Tateuchi T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five
 RT polypeptide inhibitors from the venoms of Hemachatus haemachatus
 RT (Ringhals corbra) and Naja naja (Cape cobra) and the complete amino
 RT acid sequences of two of them.";
 RU J. Biochem. 79:559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is similar to that of
 CC bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC PIR; A01316; TIRIV2.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6407 MW; 37CF03DA03D7F2A CRC64;

Query Match 58.1%; Score 198; DB 1; Length 57;
 Best Local Similarity 61.8%; Pred. No. 2,3e-17;
 Matches 34; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 3 RPDCELPADTGPCVRPSPFYNPDEKCKLEFIYGGCGGNANFTKECESTC 57
 DB 1 RPDCELPADTGPCVAKPRFYNPDEKCKLEFIYGGCGGNANFTKECESTC 55

RESULT 6
 IVD2_HEMMA STANDARD; PRT; 62 AA.
 AC P24541;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Eristocophis machaboni (Leaf-nosed viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Eristocophis.
 OC NCBI_TaxID=8702;
 RX MEDLINE=92077130; PubMed=1743283;
 RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 RT from leaf-nosed viper venom.";
 RU FEBS Lett. 294:141-143(1991).
 CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S19327; S19327.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTAS.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 2 52 BY SIMILARITY.
 FT DISULFID 11 35 BY SIMILARITY.
 FT DISULFID 27 48 BY SIMILARITY.
 FT ACT_SITE 12 13 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;

Query Match 57.2%; Score 195; DB 1; Length 62;
 Best Local Similarity 61.1%; Pred. No. 5.8e-17;
 Matches 33; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 6 FCELPADTGPCVRPSPFYNPDEKCKLEFIYGGCGGNANFTKECESTCA 59
 DB 1 FCELPADTGPCVAKPRFYNPDEKCKLEFIYGGCGGNANFTKECESTCA 54

RESULT 7
 IVD2_HEMMA STANDARD; PRT; 57 AA.
 AC P20229;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Venom trypsin inhibitor.
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OC NCBI_TaxID=35670;
 RX MEDLINE=91099304; PubMed=1702708;
 RA Shaqfat J., Beg O.U., Yin S.-U., Zaidi Z.H., Joernvall H.;
 RT "Primary structure and functional properties of cobra (Naja naja
 RT naja) venom Kunitz-type trypsin inhibitor.";
 RU Eur. J. Biochem. 194:337-341(1990).
 CC -1- FUNCTION: This protein inhibits trypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S13846; S13846.
 DR HSSP; P00981; IDTK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTAS.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Serine protease inhibitor.
 FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 57 AA; 6371 MW; AABFD7294ADC12A CRC64;

Query Match 56.9%; Score 194; DB 1; Length 57;
 Best Local Similarity 60.0%; Pred. No. 7e-17;
 Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 RPDCELPADTGPCVRPSPFYNPDEKCKLEFIYGGCGGNANFTKECESTC 57
 DB 1 RPDCELPADTGPCVAKPRFYNPDEKCKLEFIYGGCGGNANFTKECESTC 55

DB 1 RBPFCFLPAKGLCKAKHKAPEFYNNKDSHCQKEFYGGCGGANNRFTIDECNRTCC 55

RESULT 8

1B1_BUNFA STANDARD; PRT; 65 AA.

AC P25660;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Venom basic protease inhibitors IX and VIIIB.

OS Bungarus fasciatus (Banded Krait).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae; Elapidae; Bungarinae; Bungarus.

OX NCBI_Taxid=8613;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=83160048; PubMed=6832893;

RA Liu C.-S., Wu T.-C., Lo T.-B.;

RT "Complete amino acid sequences of two protease inhibitors in the venom of Bungarus fasciatus.";

RL Int. J. Pept. Protein Res. 21:209-215(1983).

CC -1- FUNCTION: Inhibitor of chymotrypsin.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC HSP; P00980; IDTX; Kunitz; Kunitz inhibitor domain.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

DR Serine protease inhibitor.

FT DISULFID 7 57 BY SIMILARITY.

FT DISULFID 16 40 BY SIMILARITY.

FT DISULFID 32 53 BY SIMILARITY.

FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).

FT VARIANT 63 65 MISSING (IN INHIBITOR VIIIB).

FT SEQUENCE 65 AA; 7294 MW; BA340749E194DB51 CRC64;

SQ

Query Match 56.3%; Score 192; DB 1; Length 65;

Best Local Similarity 57.6%; Pred. No. 1.4e-16;

Matches 34; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 KRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGANNRFTKECESTCA 59

DB 1 KRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGANNRFTKECESTCA 59

RESULT 9

1B1_CARCR STANDARD; PRT; 110 AA.

AC P00593;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chelonianin (Basic protease inhibitor) (RTP1).

OS Caretta caretta (Loggerhead).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Testudines; Cryptodira; Chelonioidea; Cheloniidae; Caretta.

OX NCBI_Taxid=8467;

RN [1]

RP SEQUENCE.

RC TISSUE=Egg white;

RX Kato I., Tomimaga N.;

RT "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tandem domains -- one Kunitz -- one of a new family.";

CC Fed. Proc. 38:832-832(1979).

CC -1- FUNCTION: THE FIRST DOMAIN INHIBITS TRYPSIN; THE SECOND ONE INHIBITS SUBTILISIN.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -1- SIMILARITY: Contains 1 WAP-type domain.

CC -1- CAUTION: AS THE PAPER ONLY INDICATES THE SPECIES AS "RED SEA TURTLE", THE SPECIES INDICATED HERE IS THEREFORE AN INFERENCE.

DR PIR; A01224; TITROR.

DR HSP; P00974; 6PTI.

DR InterPro; IPR002223; Kunitz_BPTI.

DR InterPro; IPR002221; WAP.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR Pfam; PF00095; Wap; 1.

DR PRINTS; PR00009; 4DISULPHCORE.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00131; KU; 1.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

DR Serine protease inhibitor; Pyroglutamate carboxylic acid. BPTI/KUNITZ INHIBITOR.

FT DOMAIN 8 58 WAP.

FT MOD_RES 63 105 PYROGLUTAMATE CARBOXYLIC ACID.

FT DISULFID 8 58 BY SIMILARITY.

FT DISULFID 17 41 BY SIMILARITY.

FT DISULFID 33 54 BY SIMILARITY.

FT DISULFID 67 92 BY SIMILARITY.

FT DISULFID 76 97 BY SIMILARITY.

FT DISULFID 80 93 BY SIMILARITY.

FT DISULFID 86 101 BY SIMILARITY.

FT ACT SITE 18 19 REACTIVE BOND (TRYPSIN).

FT SEQUENCE 110 AA; 11916 MW; 269436243813418E CRC64;

SQ

Query Match 55.4%; Score 189; DB 1; Length 110;

Best Local Similarity 53.6%; Pred. No. 5.5e-16;

Matches 30; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 2 DRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGANNRFTKECESTC 57

DB 3 DRPDFCELPAADTGPCRVRRPSPFYNNPDEKCKLEFYGGCGGANNRFTKECESTC 57

RESULT 10

ISIK HELPO STANDARD; PRT; 58 AA.

AC P00954;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Helix pomatia (Roman snail) (Edible snail).

OS Helix pomatia (Roman snail) (Edible snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Stigmurethra; Helicoidea; Helicidae; Helix.

OX NCBI_Taxid=6536;

RN [1]

RP SEQUENCE.

RX MEDLINE=76043680; PubMed=1183446;

RA "The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequence determination by automated Edman degradation and mass-spectral identification of the phenylthiohydantoin.";

RT Eur. J. Biochem. 58:439-451(1975).

RL [2]

RP DISULFIDE BONDS.

RX MEDLINE=76141310; PubMed=3462;

RA Dietl T., Tschesche H.;

RT "The disulfide bridges of the trypsin-kallikrein inhibitor K from snails (Helix pomatia). Thermal inactivation and proteolysis by thermolysin.";

RT Hoppe-Seyler's Z. Physiol. Chem. 357:139-145(1976).

CC -1- FUNCTION: THIS IS ONE OF SEVERAL ISOINHIBITORS OF BROAD SPECIFICITY THAT ARE SECRETED INTO THE MUCUS OF THE SNAIL.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.


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RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=78214615; PubMed=668688;
RA Joubert F.J., Strydom D.J.;
RT "Snake venoms. The amino-acid sequence of trypsin inhibitor E of
RT Dendroaspis polylepsis polylepsis (Black Mamba) venom.";
RL Eur. J. Biochem. 87:191-198(1978).
CC -1- FUNCTION: This protein inhibits trypsin and binds transition metal
CC ions such as copper and cobalt.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01215; TIEPED.
DR HSSP; P00981; IDTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI_1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 59 AA; 6620 MW; E87BFBEC0090276 CRC64;

Query Match 52.5% Score 179; DB 1; Length 59;
Best Local Similarity 57.7%; Pred. No. 4.7e-15;
Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 6 FCELPADTGCVRVPSPFYNPDEKCLPFGCGEGNANNFTKEBCESTC 57
Db 6 FCKLPAGCPKASIPATYIMAAKCOLFHYGCKGNANFTIEKCRHAC 57

RESULT 14
TFP2_MOUSE STANDARD; PRT; 230 AA.
AC 035536;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tissue factor pathway inhibitor 2 precursor (TFPI-2).
GN TFP12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Placenta;
RX MEDLINE=97101108; PubMed=8945635;
RA Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,
RA Itoh H., Hori T., Aoki I., Miugui K., Miyazaki K.;
RT "Cloning of the cDNA encoding mouse pps/TFPI-2 and mapping of the gene
RT to chromosome 6.";
RL DNA Cell Biol. 15:947-954(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=20132652; PubMed=10669168;
RA Karana Y., Kamei S., Kujiper J.L., Foster D.C., Kiesel W.;
RT "Nucleotide sequence of the gene encoding murine tissue factor pathway
RT inhibitor-2.";
RL Thromb. Haemost. 83:141-147(2000).
CC -1- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
CC WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA. ALSO EXPRESSED
CC IN LIVER AND KIDNEY.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; D50586; BAA22585.1; -
DR EMBL; AF180353; AAF40412.1; -
DR HSSP; P12111; IKNV.
DR MGD; MGI:108543; TFP12.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI_2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Signal;
KW Blood coagulation.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 230 TISSUE FACTOR PATHWAY INHIBITOR 2.
FT DOMAIN 36 86 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 96 146 BPTI/KUNITZ INHIBITOR 2.
FT DOMAIN 156 206 BPTI/KUNITZ INHIBITOR 3.
FT ACT SITE 46 47 REACTIVE BOND (BY SIMILARITY).
FT ACT SITE 106 107 REACTIVE BOND (BY SIMILARITY).
FT ACT SITE 166 167 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 36 86 BY SIMILARITY.
FT DISULFID 45 69 BY SIMILARITY.
FT DISULFID 61 82 BY SIMILARITY.
FT DISULFID 96 146 BY SIMILARITY.
FT DISULFID 105 129 BY SIMILARITY.
FT DISULFID 121 142 BY SIMILARITY.
FT DISULFID 156 206 BY SIMILARITY.
FT DISULFID 165 189 BY SIMILARITY.
FT DISULFID 181 202 BY SIMILARITY.
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 230 AA; 26137 MW; 57BAD2B36521C7B CRC64;

Query Match 52.5% Score 179; DB 1; Length 230;
Best Local Similarity 50.9%; Pred. No. 1.9e-14;
Matches 28; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 5 DCELPADTGCVRVPSPFYNPDEKCLPFGCGEGNANNFTKEBCESTCA 59
Db 34 EICLPFLDAGCPQALIPKRYDYDRDQCKRFRNYGGCLGNANNFHSRDLCOOTCS 88

RESULT 15
TVB2_DABRU STANDARD; PRT; 60 AA.
ID TVB2_DABRU
AC P00930;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom basic protease inhibitor II (RVV-II).
DE Daboia russellii siamensis (Siamese Russell's viper) (Vipera russelli)
DE siamensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Daboia.
OX NCBI_TaxID=8708;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=75060360; PubMed=4436285;
RA Takahashi H., Iwanaga S., Kitagawa T., Hokama Y., Suzuki T.;
RT "Snake venom protease inhibitors. II. Chemical structure of
RT inhibitor II isolated from the venom of Russell's viper (Vipera
RT russelli).";

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RL	J. Biochem. 76:721-733(1974).	
CC	- FUNCTION: This inhibitor has activity similar to bovine basic	
CC	protease inhibitor.	
CC	- SUBCELLULAR LOCATION: Secreted.	
CC	- SIMILARITY: Contains 1 BPTI/kunitz inhibitor domain.	
DR	HSPB, P10646; 1ADP.	
DR	InterPro, IPRO02223; Kunitz_BPTI.	
DR	Pfam, PF00014; Kunitz_BPTI, 1.	
DR	ProDom, PD000222; Kunitz_BPTI, 1.	
DR	SMART, SM00131; KU, 1.	
DR	PROSITE, PS00260; BPTI KUNITZ_1; 1.	
DR	PROSITE, PS50279; BPTI KUNITZ_2; 1.	
KM	Serine protease inhibitor.	
FT	DISULFID 7 57	
FT	DISULFID 16 40	
FT	DISULFID 32 58	
PT	ACT SITE 17 13	
SO	SEQUENCE 60 AA; 6650 MW; 5A7DCE9554CE6A2 CRC64; REACTIVE BOND (BY SIMILARITY).	

Query Match	52.2%	Score 178	DB 15	Length 60
Best Local Similarity	53.6%	Pred No. 6.2e-15		
Matches 30, Conservative		Mismatches 21	Indels 0	Gaps 0

```
Qy      2 DRPFCFLPADTGPCRVRFPFSFYNNPEKKCLEFIYGGEGGNANNFITKEECSTC 57
        ||||| : ||| ||| : ||||| ||||| ||||| : |||
Db      2 DRPTFCLAPESGRCRGHLRIYYNLSSNCKRVFFYGGCGGNANFPETRDECRETC 57
```

Search completed: January 23, 2004, 10:25:14
Job time : 6.40141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2004, 10:21:03 ; Search time 22.2289 seconds
(without alignments)
684.925 Million cell updates/sec

Title: US-09-700-179A-8
Perfect score: 342
Sequence: 1 KDHPKFCPLPAETGSCRGKV.....CGGNANPKTIEGKSTCAA 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	96.5	83	13	Q90W98 pseudonaja
2	256	74.9	83	13	Q90W99 pseudonaja
3	225	65.8	83	13	Q90W91 pseudonaja
4	217	63.5	83	13	Q90W90 pseudonaja
5	206	60.2	83	13	Q90W96 pseudonaja
6	201	58.8	83	13	Q90W97 pseudonaja
7	201	58.8	88	13	Q90W97 pseudonaja
8	191	55.8	88	13	Q8AY42 pseudonaja
9	187	54.7	88	13	Q8AY41 pseudonaja
10	187	54.7	142	5	Q8WP12 boophyllus m
11	184	53.8	142	5	Q8WP13 boophyllus m
12	183	53.5	59	5	Q91W68 anemonia su
13	178	52.0	79	13	Q91W68 anemonia su
14	173	50.6	58	5	Q91W60 anemonia su
15	172	50.3	76	5	Q8T719 bombyx mori
16	168	49.1	267	6	Q8M134 ovine aries

17	168	49.1	506	6	Q8M133	Q8M133 ovine aries
18	164	48.0	82	5	Q8WVB4	Q8WVB4 ixodes scap
19	162	47.4	58	5	Q9TW69	Q9TW69 anemonia su
20	158	46.2	287	13	Q93424	Q93424 cyprinus ca
21	157	45.9	235	11	Q8C180	Q8C180 mus musculus
22	157	45.9	235	11	Q8BSB7	Q8BSB7 mus musculus
23	156	45.6	396	6	Q28874	Q28874 canis fam1
24	154	45.0	80	5	Q8T3S7	Q8T3S7 aeneus ven
25	154	45.0	1487	5	Q8WPV5	Q8WPV5 caenornabdi
26	154	45.0	1558	5	Q8T710	Q8T710 caenornabdi
27	154	45.0	2167	5	Q76840	Q76840 caenornabdi
28	153	44.7	984	5	Q9GON2	Q9GON2 calliacis
29	153	44.7	984	5	Q9GON1	Q9GON1 calliacis
30	152	44.4	249	5	Q16701	Q16701 caenornabdi
31	151	44.2	277	13	Q8AYE1	Q8AYE1 brachydanto
32	151	44.2	759	5	Q8T791	Q8T791 ancylostoma
33	150	43.9	167	4	Q8RE89	Q8RE89 homo sapien
34	150	43.9	224	4	Q8NAK6	Q8NAK6 homo sapien
35	148	43.3	183	6	Q9N0X5	Q9N0X5 bos taurus
36	148	43.3	230	11	Q8CFP9	Q8CFP9 rattus norv
37	146.5	42.8	113	5	Q9V508	Q9V508 drosophila
38	146	42.7	154	6	Q9N0X3	Q9N0X3 ovis aries
39	146	42.7	576	4	Q8REU8	Q8REU8 homo sapien
40	146	42.7	2225	5	Q45881	Q45881 caenornabdi
41	145	42.4	169	6	Q9N0X7	Q9N0X7 bos taurus
42	145	42.4	3198	5	Q9U8G8	Q9U8G8 manduca sex
43	144	42.1	819	5	Q19305	Q19305 caenornabdi
44	143	41.8	507	11	Q9D3K4	Q9D3K4 mus musculus
45	143	41.8	507	11	Q9J0J4	Q9J0J4 mus musculus

ALIGNMENTS

RESULT 1
Q90W98 ID Q90W98 PRELIMINARY; PRT; 83 AA.
AC Q90W98; 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Textillinn.
OS Pseudonaja textillis textillis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Masel P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filipovich I.V.;
RT "Plasma inhibitors from the Australian Brown Snake Pseudonaja
textillis textillis."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RA Filipovich I.V., Sorokina N.I., Masel P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402327; AAK95522.1; -;
DR InterPro; IPR002323; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR ProDom; PD000222; Kunitz_BPTI_1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 8983 MW; 3F28548146B8A2B CRC64;
Query Match 96.5%; Score 330; DB 13; Length 83;
Best Local Similarity 96.6%; Pred. No. 1.2e-33;
Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KDHPKCELPARTGSCGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 Db 25 KDHPKCELPADTGCGRVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 2

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textilln.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophilineae; Pseudonaja.
 OC NCBI_Taxid=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filppovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filppovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF402326; AAK95521.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9158 MW; 366E82487ACPB61 CRC64;

Query Match 74.9%; Score 256; DB 13; Length 83;
 Best Local Similarity 71.2%; Pred. No. 2e-24;
 Matches 42; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KDHPKCELPARTGSCGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 Db 25 KDHPKCELPARTGSCGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 3

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textilln.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophilineae; Pseudonaja.
 OC NCBI_Taxid=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filppovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;
 RA Filppovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF402326; AAK95519.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9173 MW; 2045850657014221 CRC64;

Query Match 65.8%; Score 225; DB 13; Length 83;
 Best Local Similarity 67.8%; Pred. No. 1.5e-20;
 Matches 40; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 1 KDHPKCELPARTGSCGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 Db 25 KDHPKCELPADTGCGRVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 4

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Textilln.
 OS Pseudonaja textilis textilis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophilineae; Pseudonaja.
 OC NCBI_Taxid=169397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filppovich I.V.;
 RT "Plasmin inhibitors from the Australian brown snake Pseudonaja
 textilis textilis."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Filppovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
 RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF402326; AAK95520.1;
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 83 AA; 9179 MW; 67E589AD27175930 CRC64;

Query Match 63.5%; Score 217; DB 13; Length 83;
 Best Local Similarity 64.4%; Pred. No. 1.5e-19;
 Matches 38; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 1 KDHPKCELPARTGSCGNVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 59
 Db 25 KDHPKCELPADTGCGRVPRFYNNADHQCCKFYGGCGGANNFKTIEBCKSTCAA 83

RESULT 5

Q90W99 PRELIMINARY; PRT; 83 AA.
 AC Q90W99; 01-DEC-2001 (TREMBlrel. 19, Created)

```

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Textillin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudonaja.
NCBI_Taxid=169397;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavina M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RT "Plasma inhibitors from the Australian brown snake Pseudonaja
RT textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavina M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF402329; AAK5348.1;
DR InterPro: IPR002223; Kunitz_BPTI.
DR PRINTS: PR00759; BASICTPASE.
DR ProDom: PD000222; Kunitz_BPTI.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
DR KQ
SQ SEQUENCE 83 AA; 9060 MW; A66DF2692864C58E CRC64;

Query Match 60.2%; Score 206; DB 13; Length 83;
Best Local Similarity 61.0%; Pred. No. 3.5e-18;
Matches 36; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 KDHPKFCFLPAETGSCGNVPRFYNNADHQCCLKRIYGGCGNANFTIEBKGSTCA 59
DB 25 KDHPKFCFLPADIPGCDPFGAFHYSPRHECIEFTYGGCGNANFTIEBKGSTCA 83

RESULT 6
QY 090W97 PRELIMINARY; PRT; 83 AA.
ID 090W97
AC 090W97;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Textillin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudonaja.
NCBI_Taxid=169397;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavina M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RT "Plasma inhibitors from the Australian brown snake Pseudonaja
RT textilis textilis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina I.N., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavina M.F.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF402329; AAK5348.1;
DR InterPro: IPR002223; Kunitz_BPTI.
DR PRINTS: PR00759; BASICTPASE.
DR ProDom: PD000222; Kunitz_BPTI.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
DR KQ
SQ SEQUENCE 83 AA; 9060 MW; A66DF2692864C58E CRC64;

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DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 83 AA; 9031 MW; 9CAA7FE390D9B191 CRC64;

Query Match 58.8%; Score 201; DB 13; Length 83;
Best Local Similarity 61.0%; Pred. No. 1.5e-17;
Matches 36; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 KDHPKFCFLPAETGSCGNVPRFYNNADHQCCLKRIYGGCGNANFTIEBKGSTCA 59
DB 25 KDHPKFCFLPADIPGCDPFGAFHYSTRDRECIETIYGGCGNANFTIEBKGSTCA 83

RESULT 7
QY 08AY43 PRELIMINARY; PRT; 88 AA.
ID 08AY43
AC 08AY43;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Kunitz inhibitor a (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
NCBI_Taxid=92438;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Teal I.H., Wang Y.M., Hsu H.Y.;
RL "Structural and functional genomics of Bungarus candidus."
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY057886; AAL30068.1;
DR NON_TER
SQ SEQUENCE 88 AA; 9606 MW; E2C089906909563D CRC64;

Query Match 58.8%; Score 201; DB 13; Length 88;
Best Local Similarity 60.3%; Pred. No. 1.6e-17;
Matches 35; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 KDHPKFCFLPAETGSCGNVPRFYNNADHQCCLKRIYGGCGNANFTIEBKGSTCA 58
DB 30 KDHPKFCFLVPPPCNANVAFYNNPRLKRCIEFTYGGCGNANFTIEBKGSTCA 87

RESULT 8
QY 08AY42 PRELIMINARY; PRT; 88 AA.
ID 08AY42
AC 08AY42;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Kunitz inhibitor b (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
NCBI_Taxid=92438;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Teal I.H., Wang Y.M., Hsu H.Y.;
RL "Structural and functional genomics of Bungarus candidus."
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY057887; AAL30069.1;
DR NON_TER
SQ SEQUENCE 88 AA; 9391 MW; 71P9F57D36E7A652 CRC64;

Query Match 55.8%; Score 191; DB 13; Length 88;
Best Local Similarity 57.9%; Pred. No. 2.8e-16;
Matches 33; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 KDHPKFCFLPAETGSCGNVPRFYNNADHQCCLKRIYGGCGNANFTIEBKGSTCA 57

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Db 30 KDRPFCNVPPGRCNANVAFYNNPRLKCIFFTYGGCGGNANFKSGCKRAC 86

RESULT 9

Q8AY41 PRELIMINARY; PRT; 88 AA.
 AC Q8AY41;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Kunitz inhibitor C (Fragment).
 OS Bungarus candidus (Malayan krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 NCBI_TaxID=92438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Tsai I.H., Wang Y.M., Hsu H.Y.;
 RT "Structural and functional genomics of Bungarus candidus";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY057888; AAL30070.1; -.
 FT NON TER
 SQ SEQUENCE 88 AA; 9659 MW; 0279950755F6B787 CRC64;

Query Match 54.7%; Score 187; DB 13; Length 88; V
 Best Local Similarity 58.6%; Pred. No. 8.7e-16;
 Matches 34; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 KDHPFCELPAETGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEEGKSTCA 58
 Db 30 KDRPFCNVPPGRCNANVAFYNNPRLKCIFFTYGGCGGNANFKTIDECQRTCA 87

RESULT 10

Q8WP12 PRELIMINARY; PRT; 142 AA.
 AC Q8WP12;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Boophilin precursor.
 OS Boophilus microplus (Cattle tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
 RA Mentelle R., Huber R., Bode W., Fuentes-Prior P.;
 RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
 RT characterization, cloning and three-dimensional model of its complex
 RT with thrombin";
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA Pereira P.J., Universidade do Porto, Oporto, Portugal.
 RL EMBL; AJ304447; CAC82583.1; -.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI_2.
 DR PRINTS; PR00759; BASICPRASE.
 DR PRODOM; PD000222; Kunitz_BPTI_2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
 KW Protease inhibitor; Serine protease inhibitor; Signal.
 FT SIGNAL
 FT CHAIN 1 15 BOOPHILIN, ISOFORM H2.
 SQ SEQUENCE 142 AA; 15538 MW; 88BP0008BD42010 CRC64;

Query Match 54.7%; Score 187; DB 5; Length 142;
 Best Local Similarity 57.4%; Pred. No. 1.4e-15;
 Matches 31; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 6 FCELPAETGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEEGKSTCA 59
 Db 20 FCRLPADGICKALIPRFYNTETGCKTFSGCGGNENNETIEECQKACGA 73

RESULT 11

Q8WP13 PRELIMINARY; PRT; 142 AA.
 AC Q8WP13;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Boophilin precursor (Cattle tick).
 OS Boophilus microplus (Cattle tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pereira P.J., Prasa D., Stuerzebecher J., Sures I., Friedrich T.,
 RA Mentelle R., Huber R., Bode W., Fuentes-Prior P.;
 RT "Boophilin is a novel Kunitz-type thrombin inhibitor isolation,
 RT characterization, cloning and three-dimensional model of its complex
 RT with thrombin";
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

Query Match 53.8%; Score 184; DB 5; Length 142;
 Best Local Similarity 55.6%; Pred. No. 3.4e-15;
 Matches 30; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 6 FCELPAETGSCGNVPRFYNNADHQCCKFYGGCGGNANFKTIEEGKSTCA 59
 Db 20 FCRLPADGICKALIPRFYNTETGCKTFSGCGGNENNETIEECQKACGA 73

RESULT 12

Q8TW8 PRELIMINARY; PRT; 59 AA.
 AC Q8TW8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE KALICLUDINE 3, ASK3.
 OS Anemonia sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoaantharia; Actinaria;
 OC Nyantheae; Actiniidae; Anemonia.
 NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=96027617; PubMed=7559645;
 RA Schweitz H., Bruhn T., Guillemaire E., Moirier D., Lancelin J.M.,
 RA Beres L., Lazdunski M.;
 RT "Kalicludines and kalieptine. Two different classes of sea anemone
 RT toxins for voltage sensitive K⁺ channels";

Query Match 53.8%; Score 184; DB 5; Length 142;
 Best Local Similarity 55.6%; Pred. No. 3.4e-15;
 Matches 30; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P31713; 1SHP.
DR InterPro; IP002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394D45 CRC64;

Query Match 53.5%; Score 183; DB 5; Length 59;
Best Local Similarity 58.8%; Pred. No. 1.8e-15;
Matches 30; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 7 CELPAETGSCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 57
Db 5 CELPKVGRCRAPPRRYNNSSRCRKYIGGCGGNANFKTIEGKVC 55

RESULT 13

ID Q91351 PRELIMINARY; PRT; 79 AA.
AC Q91351;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Dendrotoxin K (Fragment).
GN DENDROTOXIN K, DTXK.
OS Dendroaspis polylepsis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Dendroaspis.
ON NCBI_TaxID=8624;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277850; PubMed=8504088;
RA Smith L.A., Lafaye P.J., Lapointe H.P., Spain T., Dolly J.O.;
RT "Cloning and functional expression of dendrotoxin K from black mamba,
a K+ channel blocker."
RL Biotechnology 32:5692-5697(1993).
DR EMBL; S61886; AAB26898.1; -.
DR HSP; P00981; DTXK.
DR InterPro; IP002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
PT NON TER 1
SQ SEQUENCE 79 AA; 8851 MW; DCDPB9APAD7D46 CRC64;

Query Match 52.0%; Score 178; DB 13; Length 79;
Best Local Similarity 58.5%; Pred. No. 1e-14;
Matches 31; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 5 KFCLEPATGSCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 57
Db 25 KYCGLPRLRGCKRKRIPFYKMKAKCCLPFDYSGCGGNANFKTIEGKRC 77

RESULT 14

ID Q9TWGO PRELIMINARY; PRT; 58 AA.
AC Q9TWGO;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE KALICUDINE 1, ASKCI.
OS Anemonia sulcata (Snake-locks sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Myantheae; Actinellidae; Anemonia.
ON NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.

RX MEDLINE=96027617; PubMed=7559645;
RA Beres L., Lazdunski M.,
RA Schweltz H., Bryhn T., Guillemane E., Moinier D., Lancelin J.M.,
RT "Kalicudine and kalipectine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126(1995).

DR HSP; P10646; 1ADZ.
DR InterPro; IP002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6691 MW; 253B068896B4BD0D CRC64;

Query Match 50.6%; Score 173; DB 5; Length 58;
Best Local Similarity 54.7%; Pred. No. 3.2e-14;
Matches 29; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 5 KFCLEPATGSCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 57
Db 3 KDCLEPMDVGRCRASHRRYYNNSSRCRKYIGGCGGNANFKTIEGKVC 55

RESULT 15

ID Q8T7L9 PRELIMINARY; PRT; 76 AA.
AC Q8T7L9;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Kazal-type serine proteinase inhibitor 1.
GN SP11.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
ON NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21873253; PubMed=11881808;
RA Nirmala X., Mita K., Vanier V., Zurovec M., Sehna F.;
RT "Identification of four small molecular mass proteins in the silk of
Bombyx mori."
RL Insect Mol. Biol. 10:437-445(2001).
DR EMBL; AF352583; AAL63944.1; -.
DR InterPro; IP002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 76 AA; 8445 MW; AA3F97D37353A3B CRC64;

Query Match 50.3%; Score 172; DB 5; Length 76;
Best Local Similarity 54.9%; Pred. No. 5.6e-14;
Matches 28; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 7 CELPAETGSCKGNVPRFYNNADHQCCKFYGGCGGNANFKTIEGKSTC 57
Db 25 CLVITKPCGKSGPRRAYVDSBDCVCFIYGGCGGNANFKTIEGCAAC 75

Search completed: January 23, 2004, 10:27:16
Job time : 23.2289 secs

